

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: October 10, 2002, 06:17:05 ; Search time 26.4 Seconds
(without alignments)
43.677 Million cell updates/sec

Title:	US-09-629-719D-8
Perfect score:	61
Sequence:	1 XPRGGSVLVTGCG 12
scoring table:	BLOSUM62
Gapop:	10.0 , Gapext: 0.5

Searched:
283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 1579

Minimum DB seq length: 0
Maximum DB seq length: 12

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

```

PIR_71:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES							
Result No.	Score	Query Length	DB ID	Description	Qy	Match	Db
1	28	45.9	11	S60354	4 GGSVLYTGC 12	45 9%; Score 28; DB 2; Length 11;	1 GGDVHVTGCG 9
2	26	42.6	7	S15597	orf 4 rara 5'-regi	55 6%; Pred. No. 1.2e+02;	
3	24	39.3	10	A61131	retinal oxidase - rabbit (fragment)	0; Mismatches 4;	
4	24	39.3	12	A33000	hydrin 2 - bullfrog	Indels 0;	
5	23	37.7	11	YHRT	hydrin 1 - African	Gaps 0;	
6	23	37.7	11	YHOU	morphogenetic neur		
7	23	37.7	11	YHBO	morphogenetic neur		
8	23	37.7	11	YHXA	morphogenetic neur		
9	23	37.7	11	YHFHY	morphogenetic neur		
10	21	34.4	9	A60522	spasm-activating p		
11	21	34.4	9	A29477	diuretic neuropept		
12	21	34.4	11	I65331	CCK-B gastrin rece		
13	21	34.4	12	S2	nepin small chain		
14	21	34.4	12	S43170	kinein light chai		
15	20	32.8	9	A26363	cardioactive pepti		
16	20	32.8	9	S27233	c cardioactive pepti		
17	20	32.8	12	A49261	coagulation factor		
18	19	31.1	9	PC2197	zymogen granule me		
19	19	31.1	10	A55695	proteoglycan core		
20	19	31.1	12	A61309	glycoprotein hormo		
21	19	31.1	12	S65629	protoxoporphyrinogen		
22	19	31.1	12	PH0930	T-cell receptor be		
23	18	29.5	8	PT0530	T-cell receptor be		
24	18	29.5	9	B28495	compressin S - co		
25	18	29.5	9	S06375	arginine vasotocin		
26	18	29.5	9	B61364	vasotocin - common		
27	18	29.5	11	PN0169	NADH dehydrogenase		
28	18	29.5	11	PT0182	T-cell receptor be		
29	18	29.5	12	S29479	hypothetical prote		

ALIGMENTS

RESULT	Match	Score	DB	Length	Similarity	Best Local	Mismatches	Conservative	Indels	Gaps
1	45 9%; Score 28; DB 2; Length 11;	45 9%; Score 28; DB 2; Length 11;	1 GGDVHVTGCG 9	1	55 6%; Pred. No. 1.2e+02;	1 GGDVHVTGCG 9	4	0;	0;	0;

Query Match 42.6%; Score 26; DB 4; Length 7;
Best Local Similarity 83.38%; Pred. No. 2.8e+05;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 PRGGSVLVTGCG

Db 2 PRGGV 7
RESULT 3
 A;Alternate names: AVT-related peptide
 N;Contains: Arg-vasotocin
 C;Species: Rana catesbeiana (bullfrog)
 C;Date: 10-Mar-1994 #sequence_revision 10-Mar-1994 #text_change 11-Jul-1997
 C;Accession: A61131
 R;Iwamuro, S.; Hayashi, H.; Yamashita, M.; Kikuyama, S.
 Gen. Comp. Endocrinol. 84, 412-418, 1991
 A;Title: Arginine vasotocin (AVT) and AVT-related peptide are major aldosterone-releasing
 A;Reference number: A61131; MUID:92225310
 A;Accession: A61131
 Molecule type: protein
 Residues: 1-10 <IWA>
 Comment: Both the decapeptide (hydrin 2) and the amidated nonapeptide (Arg-vasotocin)
 C;Superfamily: oxytocin-neurophysin
 C;Keywords: amidated carboxyl end; neuropeptide; pituitary
 F;1/Modified site: Arg-vasotocin #status experimental <RVNS>
 F;9/Modified site: amidated carboxyl end (Gly) (amide in mature form from following glycine)
 Query Match 39.3%; Score 24; DB 2; Length 10;
 Best Local Similarity 100.0%; Pred. No. 5.6e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 PRGG 5
 Db 7 PRGG 10
RESULT 4
 A33900
 Hydrin 1 - African clawed frog
 N;Alternate names: arginine-vasotocin-related peptide; vasotocinyl-Gly-Lys
 C;Species: Xenopus laevis (African clawed frog)
 C;Date: 09-Mar-1990 #sequence_revision 09-Mar-1990 #text_change 31-Mar-1997
 C;Accession: A33900; S20176
 R;Rouille, Y.; Michel, G.; Chauvet, J.; Achar, R.
 Proc. Natl. Acad. Sci. U.S.A. 86, 5212-5215, 1989
 A;Title: Hydrins, hydrocosmotic neurohypophysial peptides: osmoregulatory adaptation in a
 A;Reference number: A33900; MUID:89315797
 A;Accession: A33900
 Status: preliminary
 Molecule type: protein
 Residues: 1-12 <ROU>
 R;Iwamuro, S.; Hayashi, H.; Kikuyama, S.
 Biochim. Biophys. Acta 1176, 143-147, 1993
 A;Title: An additional arginine-vasotocin-related peptide, vasotocinyl-Gly-Lys, in Xenopus
 A;Reference number: S30176; MUID:93200145
 A;Molecule type: protein
 A;Residues: 1-12 <IWA>
 C;Keywords: neuropeptide
 Query Match 39.3%; Score 24; DB 2; Length 12;
 Best Local Similarity 100.0%; Pred. No. 6.6e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 PRGG 5
 Db 7 PRGG 10
RESULT 5
 VHBO
 morphogenetic neuropeptide - bovine
 C;Species: Bos primigenius taurus (cattle)
 C;Date: 20-Jun-2000 #sequence_revision 20-Jun-2000 #text_change 20-Jun-2000
 C;Accession: C01427; A01427
 R;Bodenmuller, H.; Schaller, H.C.
 C;Species: Rattus norvegicus (Norway rat)

Db 2 PRGGV 7
RESULT 6
 YHBU
 morphogenetic neuropeptide - human
 C;Species: Homo sapiens (man)
 C;Date: 20-Jun-2000 #sequence_revision 20-Jun-2000 #text_change 20-Jun-2000
 C;Accession: B01427; A01427
 R;Bodenmuller, H.; Schaller, H.C.
 Nature 293, 579-580, 1981
 A;Title: Conserved amino acid sequence of a neuropeptide, the head activator, from coelenterates
 A;Reference number: A93266; MUID:82035850
 A;Accession: B01427
 A;Molecule type: protein
 A;Residues: 1-11 <BOC>
 R;Birr, C.; Zachmann, B.; Bodenmuller, H.; Schaller, H.C.
 FEBS Lett. 131, 317-321, 1981
 A;Title: Synthesis of a new neuropeptide, the head activator from hydra.
 A;Reference number: A91296; MUID:82050803
 A;Contents: annotation; synthesis
 C;Comment: The synthetic peptide was identical with the natural peptide in chemical structure
 mammalian intestine and hypothalamus.
 C;Superfamily: unassigned animal peptides
 C;Keywords: blocked amino end; growth factor; hormone; hypothalamus; intestine; neuropeptide
 F;1/Modified site: blocked amino end (Gln) (probably pyrrolidine carboxylic acid) #status experimental
 Query Match 37.7%; Score 23; DB 2; Length 11;
 Best Local Similarity 50.0%; Pred. No. 9.1e+02;
 Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 QY 2 PRGGV 9
 Db 2 PPGSKVI 9
RESULT 7
 VHBO
 morphogenetic neuropeptide - bovine
 C;Species: Bos primigenius taurus (cattle)
 C;Date: 20-Jun-2000 #sequence_revision 20-Jun-2000 #text_change 20-Jun-2000
 C;Accession: C01427; A01427
 R;Bodenmuller, H.; Schaller, H.C.

Nature 293, 579-580, 1981

A;Title: Conserved amino acid sequence of a neuropeptide, the head activator, from coelenterates

A;Reference number: A93266; MUID:82035850

A;Accession: C01427

A;Molecule type: protein

A;Residues: 1-11 <BODS>

R;Birr, C.; Zachmann, B.; Bodenmüller, H.; Schaller, H.C.

FEBS Lett. 131, 317-321, 1981

A;Title: Synthesis of a new neuropeptide, the Head activator from hydra.

A;Reference number: A91296; MUID:82050803

A;Accession: A91296

A;Contents: annotation; synthesis

A;Note: the synthetic peptide was identical with the natural peptide in chemical structure

C;Comment: This peptide was first isolated from nerve cells of hydra and was called head

C;Superfamily: unassigned animal peptides

C;Keywords: growth factor; hormone; hypothalamus

F;1/Modified site: blocked amino end; growth factor; hormone; hypothalamus; intestine; neuropeptides

F;1/Modified site: blocked amino end (Gln) (probably pyrrolidine carboxylic acid) #status experimental

Query Match

Score 23; DB 2; Length 11;

Best Local Similarity 50.0%; Pred. No. 9.1e+02;

Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 2 PRGSVLV 9

Db 2 PPGSKVI 9

RESULT 8

YHAE
morphogenetic neuropeptide - sea anemone (*Anthopleura elegantissima*)

N;Alternate names: head activator

C;Species: *Anthopleura elegantissima*

C;Date: 20-Jun-2000 #sequence_revision 20-Jun-2000 #text_change 20-Jun-2000

C;Accession: A93900; A01427

R;Schaller, H.C.; Bodenmüller, H.

Proc. Natl. Acad. Sci. U.S.A. 78, 7000-7004, 1981

A;Title: Isolation and amino acid sequence of a morphogenetic peptide from hydra.

A;Reference number: A93900

A;Accession: A93900

A;Contents: annotation; synthesis

A;Note: the synthetic peptide was identical with the natural peptide in chemical structure

C;Comment: This peptide was first isolated from nerve cells of hydra and was called head

C;Superfamily: unassigned animal peptides

C;Keywords: growth factor; hormone; neuropeptide; Pyroglutamic acid

F;1/Modified site: pyrrolidine carboxylic acid (Gln) #status experimental

Query Match

Score 23; DB 2; Length 11;

Best Local Similarity 50.0%; Pred. No. 9.1e+02;

Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 2 PRGSVLV 9

Db 2 PPGSKVI 9

RESULT 10

A60522
Sperm-activating peptide SAP-IV - sea urchin (*Diadema setosum*)

C;Species: *Diadema setosum*

C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 18-Aug-2000

C;Accession: A60522

R;Toshino, K. I.; Kurita, M.; Yamaguchi, M.; Nomura, K.; Takao, T.; Shimonishi, Y.; Su

Comp. Biochem. Physiol. B 95, 423-429, 1990

A;Title: A species specific sperm-activating peptide from the egg jelly of the sea ur

A;Reference number: A60522; MUID:90227916

A;Accession: A60522

A;Molecule type: protein

A;Residues: 1-9 <COS>

C;Superfamily: unassigned animal peptides

C;Keywords: F2-9-disulfide bonds; #status experimental

Query Match

Score 23; DB 2; Length 9;

Best Local Similarity 66.7%; Pred. No. 2.8e+05;

Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 PRGSVLV 7

Db 3 PWGGAV 8

RESULT 11

A22477
diuretic neuropeptide F1 - migratory locust

C;Species: *Locusta migratoria* (migratory locust)

C;Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 31-Dec-1993

C;Accession: A22477

R;Proux, J.P.; Miller, C.A.; Li, J.P.; Carney, R.L.; Girardie, A.; Delage, M.; Schoo

Biochem. Biophys. Res. Commun. 149, 180-186, 1987

A;Title: Identification of an arginine vasopressin-like diuretic hormone from Locusta

A;Reference number: A22477; MUID:88077077

A;Accession: A22477

A;Molecule type: protein

A;Residues: 1-9 <PRO>

A;Note: two neuropeptides, F1 and F2, were identified. F2 is an antiparallel dimer of

C;Keywords: neuropeptide

Query Match

Score 21; DB 2; Length 9;

Best Local Similarity 60.0%; Pred. No. 2.8e+05;

Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 PRGSVLV 9

Db 2 PPGSKVI 9

RESULT 9

YHAE
morphogenetic neuropeptide - Hydra attenuata

N;Alternate names: head activator

C;Species: *Hydra attenuata*

C;Date: 20-Jun-2000 #sequence_revision 20-Jun-2000 #text_change 20-Jun-2000

C;Accession: B93900; A01427

R;Schaller, H.C.; Bodenmüller, H.

Proc. Natl. Acad. Sci. U.S.A. 78, 7000-7004, 1981

A;Cross-references: EMBL:X69658; NID:9468786; PIDN:CAA49349.1; PID:9468787

Db	QY	8	LVTGC	12
	:	2	LITNC	6

RESULT
165231 12

C;Species: Homo sapiens (man)
C;Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 21-Jul-2000
C;Annotation: TIGR31

R; Miyake, A.; Biochem. Biophys. Res. Commun. 208, 230-237, 1995
A; Title: A truncated isoform of human CCK-B/gastrin

A: Accession number: 165231, NCBI: JN114414

Residues: 1-11 <RES>
Cross-references: GB:S76072; NID:913752; PIDN:AAB33740.1; PID:913753
C;Genetics:

एवं विद्या उत्तमा विद्या

Best Local Similarity 50.0%; Pred NO. 2.1e-03; Mismatches 0; Indels 0; Gaps 0

Db 4 GSNMLI 9

RESULT
S70337 13

Species:

C;Species: Brassica napus var. rapifera (Swedish turnip, rutabaga)
C;Date: 19-Mar-1998 #sequence_revision 17-Apr-1998 #text_change 07-May-1999
C;Accession: S70337
R;Neumann, G.M.; Condon, R.; Thomas, I.; Polya, G.M.
BIOCHIM BIOPHYS ACTA 1295, 23-33, 1996
TITLE: Purification and sequencing of multiple forms of Brassica napus seed napin small
A;Reference number: S70336; MUID:96283790
A;Accession: S70337
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-12 <NNDD>

Qy 2 PRGGS 6
Db 1 1 1
5 PGGGS 9

RESULT 14
S43170 kinesin light chain - human (fragment)

#sequence_name: SpecieS (human)
C;Date: 13-Jan-1995 #sequence_revision 18-Aug-2000 #text_change 18-Aug-2000
C;Accession: S43170

submitted to the EMBL Data Library, December 1992
A;Description: Promoter first exon/intron characterization and chromosomal location of t

A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-12 <CHE>

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GenCore version 4.5
OMP protein - protein search, using sw model

Run on: October 10, 2002, 06:21:20 ; Search time 17.65 Seconds
(without alignments)
26.325 Million cell updates/sec

Title: US-09-629-719D-8
perfect score: 61

Sequence: XPRGGSVLVTGC 12

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 463

Minimum DB seq length: 0

Maximum DB seq length: 12

Post-processing: Maximum Match 0%

Listing first 45 summaries

Database : SwissProt_40;*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	DB ID	Description
1	23	37.7	11 MORN_HUMAN	P01163 homo sapien
2	34.4	9	1 DNFL_LOCMT	P16339 locusta mig
3	20	32.8	9 1 NCAR_CARMA	P38556 carcius ma
4	18	29.5	9 1 CONO_CONST	P05487 conus stria
5	18	29.5	9 1 OXYT_CYPCHA	P23879 cyprinus ca
6	18	29.5	11 1 NUHL_CANIFIA	P49820 canis famili
7	17	27.9	9 1 THYF_PIG	P01255 sus scrofa
8	17	27.9	12 1 V14K_WSSV	P82006 white spot
9	16	26.2	8 1 R57_MCCIT	P33564 mycobacteri
10	16	26.2	11 1 TKNA_SCYCA	P14333 scyllorhinu
11	15	24.6	9 1 CONO_CONGE	P05486 conus geogr
12	15	24.6	9 1 NGMT_BOVIN	P29177 bos taurus
13	15	24.6	10 1 BRK_ONCMY	Q9prz1 oncorynchu
14	15	24.6	12 1 CXAL_CONTM	P0983 conus imper
15	14	23.0	9 1 OXYT_RAUGL	P42994 raja clavat
16	14	23.0	9 1 SAP_STOVA	P24047 stomopeente
17	14	23.0	10 1 TKL3_LOCMT	P30249 locusta mig
18	14	23.0	11 1 CEP1_ACHFU	P2790 achatina fu
19	14	23.0	11 1 PVKL_PERAM	P1837 periplaneta
20	13.5	22.1	12 1 UR2B_CYPCHA	P04561 cyprinus ca
21	13	21.3	7 1 CCFL_ENTFA	P20104 enterococcus
22	13	21.3	7 1 FAR2_HIRME	P42564 hirudo medi
23	13	21.3	8 1 CAD1_ENTFA	P13268 enteroecocco
24	13	21.3	8 1 UF06_MOUSE	P38644 mus musculu
25	13	21.3	9 1 ISOF_CYPCHA	P42993 cyprinus ca
26	13	21.3	10 1 ESTA_SCHGCA	P81012 schizaphis
27	13	21.3	10 1 PAPL_PARMA	P18863 pardachirus
28	13	21.3	10 1 TPIS_NICPL	P19118 nicotiana p
29	13	21.3	10 1 URA1_HUMAN	P32118 homo sapien
30	13	21.3	11 1 BPP4_BOTTN	P10424 bothrops in
31	13	21.3	11 1 PKCL_CARMO	P82684 carausius m
32	13	21.3	11 1 RE41_LITRU	P82074 litoria rub
33	13	21.3	12 1 PSP3_PHYPKA	P80662 physcomitri

ALIGNMENTS

RESULT	1	MORN_HUMAN	STANDARD;	PRT;	11 AA.
ID	MORN_HUMAN				
AC	P01163;				
DT	21-JUL-1986 (Rel. 01, Created)				
DT	21-JUL-1986 (Rel. 01, Last sequence update)				
DT	01-OCT-1995 (Rel. 34, Last annotation update)				
DE	Morphogenetic neuropeptide (Head activator) (HA).				
OS	Homo sapiens (Human),				
OS	Rattus norvegicus (Rat),				
OS	Bos taurus (Bovine),				
OS	Anthopleura elegantissima (Sea anemone), and				
OC	Hydra attenuata (Hydra) (Hydra vulgaris), and				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OX	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
RN	[1]				
RP	SEQUENCE.				
RC	SPECIES=Human, Rat, and Bovine;				
RX	MEDLINE=82035850; PubMed=7290191;				
RA	Bodenmüller H., Schaller H.C.;				
RT	"Conserved amino acid sequence of a neuropeptide, the head activator, from coelenterates to humans.";				
RL	Nature 293:579-580(1981).				
RN	[2]				
RP	SEQUENCE.				
RC	SPECIES=A.elegansissima, and H.attenuata;				
RA	Schaller H.C., Bodenmüller H.;				
RT	"Isolation and amino acid sequence of a morphogenetic peptide from Hydra.;"				
RT	Proc. Natl. Acad. Sci. U.S.A. 78:7000-7004(1981).				
RL	[3]				
RN	SYNTHESIS.				
RP	MEDLINE=82050803; PubMed=7297679;				
RX	Birr C., Zachmann B., Bodenmüller H., Schaller H.C.;				
RA	"Synthesis of a new neuropeptide, the head activator from hydra.;"				
RT	FEMS Lett. 131:317-321(1981).				
RL	[4]				
RN	FUNCTION.				
RP	MEDLINE=90059923; PubMed=2283101;				
RX	Schaller H.C., Druffel-Augustin S., Dubel S.;				
RA	"Head activator acts as an autocrine growth factor for NH15-CA2 cells in the G2/mitosis transition."				
RT	EMBO J. 8:3311-3318(1989).				
RL	-1- FUNCTION: HA ACTS AS AN AUTOCRINE GROWTH FACTOR FOR NEURAL CELLS				
CC	IN THE G2/MITOSES TRANSITION.				
CC	-1- CAUTION: THIS PEPTIDE WAS FIRST ISOLATED FROM NERVE CELLS OF HYDRA AND WAS CALLED HEAD ACTIVATOR BY THE AUTHORS, BECAUSE IT INDUCED HEAD-SPECIFIC GROWTH AND DIFFERENTIATION IN THIS ANIMAL. IT HAS BEEN FOUND IN MAMMALIAN INTESTINE AND HYPOTHALAMUS.				
DR	PIR; B01427; YHNU.				
DR	A01427; YHNU.				
DR	C01427; YHNU.				
DR	A93900; YHXA.				
DR	PIR; B93900; YHJFV.				
KW	Growth factor; Cell cycle; Mitosis.				

FT	MOD_RES	1	1	PYRROLIDONE CARBOXYRIC ACID.	OC	Subrachyura; Portunoidea; Portunidae; Carcinus.
SQ	SEQUENCE	11 AA;	1142 MW;	37927417C325B878 CRC64;	OX	NCBI-TaxID=6759, 7130, 7067, 37547;
Query Match	Score	37.7%	DB 1;	Length 11;	RN	[1]
Best Local Similarity	50.0%	Pred. No.	3.9e-02;		RP	SEQUENCE.
Matches	4;	Conservative	2;	Mismatches	RA	SPECIES="C.menaas"; TISSUE="Pericardial organs;"
Qy	2 PRGSVLV 9		2;	Indels	RA	"unusual cardioactive peptide (CCAP) from pericardial organs of the
Db	2 PPGSCKV 9		0;	Gaps	RT	shore crab <i>Carcinus maenas</i> ;"
			0;		RL	Proc. Natl. Acad. Sci. U.S.A. 84:575-579(1987).
RESULT	2				RN	[2]
ID	DNFL_LOCHI	STANDARD;	PRT:	9 AA.	RP	SEQUENCE.
AC	P16339;				RC	SPECIES="M.sexata";
	01-AUG-1990 (Rel. 15, Created)				RC	"Primary structure of a cardioactive neuropeptide from the tobacco
	01-AUG-1990 (Rel. 15, Last sequence update)				RC	hawkmoth, <i>Manduca sexta</i> ;"
DE	Locupressin (Diuretic neuropeptide F1/F2).				RL	FEBS Lett. 313:165-168(1992).
OS	Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;				RN	[3]
OC	Pterygota; Neoptera; Orthopteroidea; Orthoptera; Caelifera;				RP	SEQUENCE.
OC	Acridoidea; Acridiidae; Locusta.				RA	Medline=9305043; Pubmed=1426284;
OC	Acridomorpha; Acridoidea; Acriidae; Locusta.				RA	Cheung C.C., Loi P.K., Sylvester A.W., Lee T.D., Tublitz N.J.;
OX	NCBI-TaxID=7004;				RT	"Primary structure of a cardioactive neuropeptide from the tobacco
RN	[1]				RC	hawkmoth, <i>Manduca sexta</i> ;"
RP	SEQUENCE.				RC	Medline=94176032; Pubmed=8128851;
RC	TISSUE=>SUBEOESOPHAGEAL ganglion, and Thoracic ganglion;				RC	Furuya K., Liso S., Reynolds S.E., Ota R.B., Hackett M.,
RX	MEDLINE=>8807077; PubMed=3688410;				RA	"Isolation and identification of a cardioactive peptide from <i>Tenebrio molitor</i> and <i>Spodoptera eridania</i> ;"
RX	PIROU J.P., MILLER C.A., LI J.-P., CARNEY R.L., GIRARDIE A. /				RA	Biol. Chem. Biopolymers 374:1065-1074(1993).
RT	"Identification of an arginine vasopressin-like diuretic hormone from				CC	-i- FUNCTION: THE EFFECT OF CCAP IS BOTH INO- AND CHRONOTROPIC.
RT	Locusta migratoria;"				CC	-i- TISSUE SPECIFICITY: STORED IN PERICARDIAL ORGANS AND RELEASED INTO THE HEMOLYMPH.
RL	Biochem. Biophys. Commun. 149:180-186(1987).				DR	DR: A26363; A26363.
CC	-i- FUNCTION: DIURETIC HORMONE.				DR	PIR: S27333; S27233.
CC	-i- SUBUNIT: F2 IS AN ANTIPARALLEL DISULFIDE LINKED DIMER OF F1.				FT	Neuropeptide; Amidation.
CC	-i- SIMILARITY: BELONGS TO THE VASOPRESSIN/OXYTOCIN FAMILY.				FT	DISULFID: 3 DISULFID
DR	PIR: A29477, A29477.				FT	AMIDATION.
DR	Interpro: IPR000981; Neurhypophys_horm.				FT	DISULFID: 3 DISULFID
DR	Pfam: PF0220; hormone4; 1.				FT	AMIDATION.
DR	PROSITE: PS00264; NEUROHYPOPHYS_HORM; 1.				FT	MOD_RES 9 9 9 AMIDATION.
KW	Hormone; Neuropeptide; Amidation.				FT	SEQUENCE 9 AA; 959 MW; C5A861AQCD44EB9 CRC64;
FT	DISULFID 1 1 INTERCHAIN (WITH C-6') (IN F2) .				FT	Query Match
FT	DISULFID 1 1 INTERCHAIN (WITH C-1') (IN F2) .				FT	Best Local Similarity 32.8%; Score 20; DB 1; Length 9;
FT	DISULFID 6 6 AMIDATION.				FT	Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
FT	MOD_RES 9 SEQUENCE 9 AA; 976 MW; 56EB176EB45JA057 CRC64;				FT	Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
RESULT	4				FT	Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
ID	CONO CONST	STANDARD;	PRT:	9 AA.	FT	Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
AC	P05487;				FT	Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
AC	01-NOV-1988 (Rel. 09, Created)				FT	Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DT	01-Oct-1994 (Rel. 10, Last sequence update)				FT	Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DT	01-Nov-1994 (Rel. 09, Last sequence update)				FT	Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DT	01-Nov-1995 (Rel. 32, Last annotation update)				FT	Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DE	Arg-conopeptin S.				FT	Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OS	Conus striatus (Striated cone).				FT	Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OC	Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;				FT	Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OC	Neogastropoda; Conoidea; Conidae; Conus.				FT	Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OX	NCBI-TaxID=6493;				FT	Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
RN	[1]				FT	Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
RP	SEQUENCE.				FT	Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
RX	Medline=98058932; PubMed=3680228;				FT	Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
RX	RUA CRUZ L.J., de Santos V., Zafaralla G.C., Ramilo C.A., Zeikus R.D.,				FT	Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
RX	Gray W.R., Olivera B.M.; Cruz L.J.;				FT	Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
RX	"Invertebrate vasopressin/oxytocin homologs. Characterization of peptides from <i>Conus geographus</i> and <i>Conus striatus</i> venoms.";				FT	Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
RX	J. Biol. Chem. 262:15821-15824(1987).				FT	Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
RN	[2]				FT	Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
RP	REVIEW.				FT	Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
RX	Medline=99024586; PubMed=3052286;				FT	Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
RX	Gray W.R., Olivera B.M., Cruz L.J.;				FT	Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
RX	"Peptide toxins from venomous <i>Conus</i> snails.";				FT	Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
RX	Annu. Rev. Biochem. 57:665-700(1988).				FT	Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CC	-i- SIMILARITY: BELONGS TO THE VASOPRESSIN/OXYTOCIN FAMILY.				FT	Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DR	PTR; 438495; B28495.	ID	NUHM_CANFA	STANDARD;	PRM;	11 AA.
DR	InterPro; IPR00081; Neurhypophys_horm.	AC	P49820;			
DR	PFAM; PF00220; hormone4; 1.	DT	01-OCT-1996 (Rel. 34, Created)			
DR	PROSITE; PS0264; NEUROHYPOPHYS_HORM; 1.	DT	15-JUL-1998 (Rel. 36, Last sequence update)			
KW	Hormone; Amidation.	DT	15-JUL-1999 (Rel. 38, Last annotation update)			
FT	DISULFID 1	DE	NADH-ubiquinone oxidoreductase 24 kDa subunit (EC 1.6.5.3)			
FT	MOD_RES 9 9 AMIDATION.	DE	(EC 1.6.99.3). (Fragment).			
SQ	SEQUENCE 9 AA; 1031 MW; 17EB176EB4540050 CRC64;	GN	NDUFV2.			
Query Match	29.5%; Score 18; DB 1; Length 9;	OS	Canis familiaris (Dog).			
Best Local Similarity	100.0%; Pred. No. 1e+05;	OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
Matches	0; Mismatches 0; Indels 0; Gaps 0;	OC	Mammalia; Eutheria; Carnivora; Pisipedia; Canidae; Canis.			
QY	2 PRG 4	OX	NCBI_TaxID=9015;			
Db	7 PRG 9	RN	[1]			
RESULT	5	RP	SEQUENCE.			
OXT_CTPCA		RC	TISSUE-Heart;			
ID	OXT_CTPCA STANDARD; PRT; 9 AA.	RA	MEIDLINE=98163340; PubMed=9504812;			
P23879;		RA	Dunn, M.J., Corbett, J.M., Wheeler, C.H.;			
01-NOV-1991 (Rel. 20, Last sequence update)		RT	"NSC-20PAGE and the two-dimensional gel electrophoresis database of			
01-NOV-1995 (Rel. 32, Last annotation update)		RT	dog heart proteins.";			
DE	Vasotocin.	RL	Electrophoresis 18:2795-2802(1997).			
OS	Cyprinus carpio (Common carp), and	CC	-I - FUNCTION: TRANSFER OF ELECTRONS FROM NADH TO THE RESPIRATORY			
OS	Petromyzon marinus (Sea lamprey),	CC	CHAIN. THE IMMEDIATE ELECTRON ACCEPTOR FOR THE ENZYME IS BELIEVED			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	CC	TO BE UBIQUINONE. COMPONENT OF THE FLAVOPROTEIN-SULFUR (FP)			
OC	Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;	CC	FRAGMENT OF THE ENZYME.			
OC	Cypriniformes; Cyprinidae; Cyprinus.	CC	-I - CATALYTIC ACTIVITY: NADH + ubiquinone = NAD(+)+ ubiquinol.			
NCBI_TaxID=7962, 7757;		CC	-I - COFACTOR: 2Fe-2S IRON-SULFUR CLUSTER N 1B.			
RN	[1]	CC	-I - SUBUNIT: COMPLEX I IS COMPOSED OF ABOUT 40 DIFFERENT SUBUNITS.			
RP	SEQUENCE=C. carpio; TISSUE=Pituitary;	CC	THIS IS A COMPONENT OF THE FLAVOPROTEIN FRACTION.			
RA	Acher, R.; Chauvet, J.; Chauvet, M.-T.; Crepy, D.;	CC	-I - SUBCELLULAR LOCATION: MATRIX AND CYTOPLASMIC SIDE OF THE			
RT	"Characterization of neurohypophyseal hormones from a fresh water bony	CC	MITOCHONDRIAL INNER MEMBRANE.			
RT	fish, the carp (Cyprinus carpio). Comparison with hormones from sea	CC	-I - SIMILARITY: BELONGS TO THE COMPLEX I 24 kDa SUBUNIT FAMILY.			
RL	water bony fishes"; Comp. Biochem. Physiol. 14:245-254(1965).	DR	DR-2DPAGE; P49820; DOG.			
RN	[2]	DR	InterPro; IPR02023; Complex1_24K.			
RP	SEQUENCE.	DR	PROSITE; PS01099; Complex1_24K; PARTIAL.			
RC	SPECIES=P. marinus; TISSUE=Pituitary;	FT	Oxidoreductase; NAD; ubiquinone; Mitochondrion; Iron-sulfur.			
RX	MEDLINE=88225976; PubMed=3371648;	FT	NON_TER 11 11			
RA	Lane, T. F., Sower, S.A., Kawauchi, H.;	SEQUENCE 11 AA; 1099 MW; 267F5369C9C72DBB CRC64;				
RT	"Arginine vasotocin from the pituitary gland of the lamprey (Petromyzon marinus): isolation and amino acid sequence.";	SO				
RT	Gen. Comp. Endocrinol. 70:152-157(1988).					
CC	-I - FUNCTION: ANGIOTENSIN II RECEPTOR.					
CC	-I - SIMILARITY: BELONGS TO THE VASOPRESSIN/OXYTOCIN FAMILY.					
PIR; B61364;	B61364.					
PIR; S06375;	S06375.					
DR	InterPro; IPR009881; Neurohypophys_horm.					
DR	PFAM; PF00220; hormone4; 1.					
DR	PROSITE; PS0264; NEUROHYPOPHYS_HORM; 1.					
KW	Hormone; Amidation.					
FT	DISULFID 1 6					
FT	MOD_RES 9 9 AMIDATION.					
SQ	SEQUENCE 9 AA; 1053 MW; 17EB176EB4540048 CRC64;					
RN	[1]					
Query Match	29.5%; Score 18; DB 1; Length 9;	RP	SEQUENCE.			
Best Local Similarity	100.0%; Pred. No. 1e+05;	RX	MEDLINE=78026571; PubMed=914862;			
Matches	0; Mismatches 0; Indels 0; Gaps 0;	RA	Plein, J.-M., Dardenne, M., Blouquit, Y., Bach, J.-F.,			
QY	2 PRG 4	RT	"Structural study of circulating thyminic factor: a peptide isolated from pig serum. II. Amino acid sequence.";			
Db	7 PRG 9	RL	J. Biol. Chem. 252:8045-8047(1977).			
RESULT	6	CC	-I - MISCELLANEOUS: THE BIOLOGICAL SOURCE(S) AND PHYSIOLOGICAL			
NUHM_CANFA		CC	ACTIVITIES OF THIS PEPTIDE HAVE NOT BEEN DETERMINED.			
FT	MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.	DR	PIR; A01523; YFFG.			
SQ	SEQUENCE 9 AA; 876 MW; D500B87166C5B33D CRC64;	FT	MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.			

Query Match 27.9%; Score 17; DB 1; Length 9;
 Best Local Similarity 75.0%; Pred. No. 1e+05;
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 RGG 6
 AC :|||
 Db 5 QGG 8

RESULT 8
 V14K_WSSV STANDARD; PRT; 12 AA.
 ID V14K_WSSV
 AC PB2006;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 RL 14.5 kDa structural polyprotein (Fragment).
 CC -I- FUNCTION: STRUCTURAL COMPONENT OF THE VIRION.
 FT NON_TER 12 12
 SEQUENCE 12 AA; 1242 MW; 24B8DE4FFD21A338 CRC64;

Query Match 27.9%; Score 17; DB 1; Length 12;
 Best Local Similarity 100.0%; Pred. No. 4.2e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RN [1]
 RP STRAIN=South Carolina;
 RX MEDLINE-20214217; PubMed=10752552;
 RA Wang Q., Poulos B. T., Lighter D. V.;
 RT "Protein analysis of geographic isolates of shrimp white spot syndrome virus.";
 RL Arch. Virol. 145:263-274 (2000).
 CC -I- FUNCTION: STRUCTURAL COMPONENT OF THE VIRION.
 FT NON_TER 12 12
 SEQUENCE 12 AA; 1242 MW; 24B8DE4FFD21A338 CRC64;

Query Match 26.2%; Score 16; DB 1; Length 8;
 Best Local Similarity 75.0%; Pred. No. 1e+05;
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 PRGG 5
 AC :|||
 Db 1 PRKG 4

RESULT 10
 TKNA_SCYCA STANDARD; PRT; 11 AA.
 ID TKNA_SCYCA
 AC P41333;
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DE Substance_P.
 CC Scyliorhinus canicula (Spotted dogfish) (Spotted catshark);
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chonrichthyes;
 OC Elasmobranchii; Galeomorphi; Galeoidea; Carcharhiniformes;
 OC Scyliorhinidae; Scyliorhinus.
 OX NCBI-TaxID=7830;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Brain;
 RX MEDLINE-9329508; PubMed=7685693;
 RA Waugh D., Wang Y., Hazon N., Balment R.J., Conlon J.M.;
 RT "Primary structures and biological activities of substance-P-related peptides from the brain of the dogfish, *Scyliorhinus canicula*."
 RL Eur. J. Biochem. 214:469-474(1993).
 CC -I- EVOKE BEHAVIORAL RESPONSES, ARE POTENT VASODILATORS AND SECRETAGOGUES, AND CONTRACT (DIRECTLY OR INDIRECTLY) MANY SMOOTH MUSCLES.
 CC -I- SIMILARITY: BELONGS TO THE TACHYKININ FAMILY.
 DR PIR: S33300; S33300.
 DR InterPro: IPR003580; Prototachykinin.
 DR InterPro: IPR002040; Tachykinin.
 DR Pfam: PF02202; Tachykinin_1.
 DR SMART: SM00203; TK_1.
 DR PROSITE: PS00267; TACHYKININ_1.
 KW Tachykinin; Neuropeptide; Amidation; Neurotransmitter.
 FT MOD_RES 11 11
 SEQUENCE 11 AA; 1278 MW; 24B860DEC9D6D867 CRC64;

RN [1]
 RP SEQUENCE FROM N.A.

RX MEDLINE-93197130; PubMed=8451173;

RA Nair J., Rouse D.A., Morris S.L.;
 RT "Nucleotide sequence analysis of the ribosomal S12 gene of Mycobacterium intracellulare";
 RL Nucleic Acids Res. 21:1031-1039(1993).
 CC -I- FUNCTION: PROTEIN S7 BINDS SPECIFICALLY TO PART OF THE 3' END OF 16S RIBOSOMAL RNA (BY SIMILARITY).

CC -I- SIMILARITY: BELONGS TO THE S7P FAMILY OF RIBOSOMAL PROTEINS.

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CC or send an email to license@isb-sib.ch).

CC -----

DR EMBL; L08171; AAA25376.1; -.

DR PIR; S35538; S35538.

DR InterPro; IPR00235; Ribosomal_S7.

DR PROSITE; PS00052; RIBOSOMAL_S7; PARTIAL.

KW Ribosomal protein; rRNA-binding.

FT INIT_MET 0 0 BY SIMILARITY.

FT NON_TER 8 8

SQ SEQUENCE 8 AA; 850 MW; 63276DC768732417 CRC64;

RESULT 11
 CONO_CONGE STANDARD; PRT; 9 AA.
 ID CONO_CONGE
 AC P05846;
 DT 01-NOV-1988 (Rel. 09, Created)

Query Match 26.2%; Score 16; DB 1; Length 11;
 Best Local Similarity 75.0%; Pred. No. 5.7e+03;
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 PRGG 5
 AC :|||
 Db 2 PRPG 5

DT 01-NGV-1995 (Rel. 32, Last annotation update)

DE LYS-conpressin G.

OS Conus geographus (Geography cone).

OC Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;

OC Neogastropoda; Conoidea; Conidae; Conus.

OX NCBI_TaxID=6491;

RN [1]

RP SEQUENCE.

RX MEDLINE=88058932; PubMed=3680228;

RA Cruz L.J., de Santos V., Zafaralla G.C., Ramilo C.A., Zeikus R.D., Gray W.R., Olivera B.M.;

RT "Invertebrate vasoressin/oxytocin homologs. Characterization of peptides from Conus geographus and conus straitus venoms.";

RL J. Biol. Chem. 262:15821-15824 (1987).

RN [2]

RP REVIEW.

RX MEDLINE=89024586; PubMed=3052286;

RA Gray W.R., Olivera B.M., Cruz L.J.;

RT "Peptide toxins from venomous conus snails.";

RL Ann. Rev. Biochem. 57:665-700 (1988).

CC -!- SIMILARITY: BELONGS TO THE VASOPRESSIN/OXYTOCIN FAMILY.

DR PIR: A28495; A28495.

InterPro: IPR00081; Neurhypophys_horm.

PRAM: PRF0220; hormone4_1.

PROSITE: PS00264; NEUROHYPOPHYS_HORM: 1.

FT DISULFID 1

FT MOD_RES 9 9 AMIDATION

SQ SEQUENCE 9 AA; 1037 MW; D4FC276EB4540059 CRC64;

Query Match 24.6%; Score 15; DB 1; Length 9;

Best Local Similarity 66.7%; Pred. No. 1e-05;

Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 7 PKG 9

QY 2 PRG 4

l:l

RESULT 12

MGMNT_BOVIN STANDARD; PRT; 9 AA.

AC P29177;

DT 01-DEC-1992 (Rel. 24, Created)

DT 01-DEC-1992 (Rel. 24, Last sequence update)

DT 01-OCT-1996 (Rel. 34, Last annotation update)

DE Methylated-DNA-protein-cysteine methyltransferase (EC 2.1.1.63) (6-O-methylguanine-DNA methyltransferase) (Fragment).

GN MGMN

BS taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Detartoiodactyla; Ruminantia; Pecora; Bovoidea; Bovidae; Bovinae; Bos.
NCBI_TaxID=9913;

RN [1]

RP SEQUENCE.

RC TISSUE="Thymus";

RX MEDLINE=90174912; PubMed=2308822;

RA Rydberg B., Hall J., Karren P.;

RT "active site amino acid sequence of the bovine O6-methylguanine-DNA methyltransferase"; Nucleic Acids Res. 18:17-21 (1990).

RL -!- FUNCTION: REPAIR OF ALKYLATED GUANINE IN DNA BY STOICHIOMETRICALLY TRANSFERRING THE ALKYL GROUP AT THE O-6 POSITION TO A CYSTEINE RESIDUE IN THE ENZYME. THIS IS A SUICIDE REACTION: THE ENZYME IS IRREVERSIBLY INACTIVATED.

CC -!- CATALYTIC ACTIVITY: DNA (containing 6-O-methylguanine) + (protein-L-cysteine) = DNA (without 6-O-methylguanine) + protein S-methyl-L-cysteine.

CC -!- SIMILARITY: WITH SEGMENTS OF E.COLI ADA AND OGT METHYLTRANSFERASE WHICH ENCOMPASS THE ALKYL-ACCEPTOR RESIDUES.

DR InterPro; IPR001497; Methyltransf_1.

Query Match 24.6%; Score 15; DB 1; Length 9;

Best Local Similarity 40.0%; Pred. No. 1e-05;

Matches 2; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Db 5 ILTPC 9

QY 8 LYTGIC 12

l:l

RESULT 13

BRK_ONCNY STANDARD; PRT; 10 AA.

ID BRK_ONCNY

AC Q9PRZ1;

CC -!- SIMILARITY: BELONGS TO THE VASOPRESSIN/OXYTOCIN FAMILY.

DR 16-OCT-2001 (Rel. 40, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Lysyl-bradykinin-like.

OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Protacanthopterigii; Salmoniformes; Salmonidae; Oncorhynchus.

OX NCBI_TaxID=8022;

RN [1]

RP SEQUENCE.

RX MEDLINE=94039817; PubMed=8224232;

RA Conlon J.M., Olson K.R.;

RT "Purification of a vasoactive peptide related to lysyl-bradykinin from trout plasma.";

RL FEBS Lett. 334:75-78 (1993).

CC -!- FUNCTION: SMOOTH MUSCLE CONTRACTION. PROBABLY PLAYS A ROLE FOR THIS SYSTEM IN CARDIOVASCULAR REGULATION IN FISH.

CC -!- SUBCELLULAR LOCATION: Secreted.

CC -!- TISSUE SPECIFICITY: PLASMA.

CC -!- SIMILARITY: BELONGS TO THE BRADYKININ FAMILY.

CC Bradykinin; Vasodilator.

KW SEQUENCE 10 AA; 1193 MW; 33C59075A3786777 CRC64;

Query Match 24.6%; Score 15; DB 1; Length 10;

Best Local Similarity 57.1%; Pred. No. 7.7e+03;

Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Db 3 PRGWSPL 9

QY 2 PRGGSVL 8

l:l

RESULT 14

CXAL_CONIM STANDARD; PRT; 12 AA.

ID CXAL_CONIM

AC P50983;

CC -!- SIMILARITY: BELONGS TO THE VASOPRESSIN/OXYTOCIN FAMILY.

DR 01-OCT-1996 (Rel. 34, Created)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Alpha-conotoxin Im1.

OS Conus imperialis (Imperial cone).

OC Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda; Neogastropoda; Conoidea; Conidae; Conus.

OX NCBI_TaxID=35631;

RN [1]

RP SEQUENCE, AND SYNTHESIS.

RC TISSUE="Venom";

RX MEDLINE=94256889; PubMed=8206995;

RA McIntosh J.M., Yoshikami D., Mahe E., Nielsen D.B., Rivier J.E., Gray W.R., Olivera B.M.;

RT "A nicotinic acetylcholine receptor ligand of unique specificity,
alpha-conotoxin ImI.";
RT J. Biol. Chem. 269:16733-16739(1994).
RN [2]
RP CHARACTERIZATION.
RX MEDLINE:95319776; PubMed=7651351;
RA Johnson D.S., Martinez J., Elgozhen A.B., Heinemann S.F.,
RA McIntosh J.M.;
RT "Alpha-conotoxin ImI exhibits subtype-specific nicotinic
acetylcholine receptor blockade: preferential inhibition of homomeric
alpha 7 and alpha 9 receptors.";
RL Mol. Pharmacol. 48:194-199(1995).
RN [3]
RP STRUCTURE BY NMR.
RX MEDLINE:99212205; PubMed=10194298;
RA Rogers J.P., Luginbuhl P., Shen G.S., McCabe R.T., Stevens R.C.,
Weintraub D.E.;
"NMR solution structure of alpha-conotoxin ImI and comparison to
other conotoxins specific for neuronal nicotinic acetylcholine
receptors.";
RL Biochemistry 38:3874-3882(1999).
RN [4]
RP STRUCTURE BY NMR.
RX MEDLINE:9915061; PubMed=10050774;
RA Maslennikov I.V., Shentarev Z.O., Zhuk M.N., Ivanov V.T.,
Metressel C., Tselelin V.I., Arseniev A.S.,
"NMR spatial structure of alpha-conotoxin ImI reveals a common
scaffold in snail and snake toxins recognizing neuronal nicotinic
acetylcholine receptors.";
RL FEBS Lett. 444:275-280(1999).
RN [5]
RP STRUCTURE BY NMR.
RX MEDLINE:99324017; PubMed=10395477;
RA Gehrmann J., Daly N.L., Alewood P.F., Craik D.J.;
"Solution structure of alpha-conotoxin ImI by ¹H nuclear magnetic
resonance.";
RT J. Med. Chem. 42:2364-2372(1999).
CC FUNCTION: ALPHA CONOTOXINS ACT ON POSTSYNAPtic MEMBRANES, THEY
BIND TO THE NICOTINIC ACETYLCHOLINE RECEPTORS (NACHR) AND THUS
INHIBIT THEM. IT IS HIGHLY ACTIVE AGAINST THE NEUROMUSCULAR
RECEPTOR IN FROG BUT NOT IN MICE. IN CONTRAST, IT INDUCES SEIZURES
WHEN INJECTED CENTRALLY IN MICE AND RATS. IT TARGET NEURONAL
NACHRs IN MAMMALS. BLOCKS HOMOMERIC ALPHA-7 NICOTINIC RECEPTORS
WITH THE HIGHEST APPARENT AFFINITY AND HOMOMERIC ALPHA-9 RECEPTORS
WITH 8-FOLD LOWER AFFINITY. HAS NO EFFECT ON RECEPTORS COMPOSED OF
ALPHA-2/BETA-2, ALPHA-3/BETA-2, ALPHA-4/BETA-2, ALPHA-2/BETA-4,
ALPHA-3/BETA-4, OR ALPHA-4/BETA-4 SUBUNIT COMBINATIONS.
CC -1- SIMILARITY: BELONGS TO THE ALPHA-TYPE CONOTOXIN FAMILY.
DR PDB: 1IMI; 15-JUN-99.
DR PDB: 1IMI; 23-APR-99.
DR PDB: 1CNU; 27-MAY-99.
KW Postsynaptic neurotoxin;
KW Acetylcholine receptor inhibitor; Amidation;
KW 3D-structure.
CC -1- SUBCELLULAR LOCATION: Secreted.

-1- DISULFID 2 8

-1- DISULFID 3 12

SEQUENCE 12 AA; 1357 MW; 9C29CEA545A4176A CRC64;

Query Match 23.0%; Score 14; DB 1; Length 9;
Best Local Similarity 66.7%; Pred. No. 1e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Job time: 356 sec

Qy	11 GC 12	Db	1 GC 2
RESULT	15	OXT_RAJCL	
ID		OXT_RAJCL	STANDARD:
AC	P42994;		PRT:
			9 AA.

Query Match 23.0%; Score 14; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 9e+03; Mismatches 0; Indels 0; Gaps 0;
Matches 2; Conservative 0; Mismatches+0; Indels 0; Gaps 0;

DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Glumictocin.
OS Raja clavata (Thornback ray).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
Elasmobranchii; Squalea; Hypnosqualea; Pristiorajea; Batoidea;
Rajiformes; Rajidae; Raja.
OX NCBI_TaxID=7781;
RN [1]
RP SEQUENCE.
RX MEDLINE:66123415; PubMed=5880565;
RA Achter R., Chauvet J., Chauvet M.-T., Crepy D.;
RT "Phylogeny of neurohypophyseal peptides: Isolation of a new hormone,
glumictocin (Ser 4-Gln 8-oxytocin) present in a cartilaginous fish,
the ray (Raja clavata).";
RT Pfam: PRO00981; Neurhypophys_horm.
RL Biochim. Biophys. Acta 107:393-396(1965).
CC -1- FUNCTION: ANTIDIUREtic HORMONE.
-1- SIMILARITY: BELONGS TO THE VASOPRESSIN/OXYTOCIN FAMILY.
DR Interpro; IPRO00981; Neurhypophys_horm.
DR Pfam: PRO00220; hormone4; 1.
DR PROSITE; PS00264; NEUROHYPOPHYS_HORM; 1.
KW Hormone; Amidation.
FT DISTIFID 1 MOD_RES 9 AMIDATION
FT SEQUENCE 9 AA; 984 MW; 17E9C76EB455B04B CRC64;

Query Match 23.0%; Score 14; DB 1; Length 9;

Best Local Similarity 66.7%; Pred. No. 1e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 PRG 4
Db 7 PQG 9

Search completed: October 10, 2002, 06:21:20

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: October 10, 2002, 06:23:38 ; Search time 43.8 Seconds

(without alignments)
47.396 Million cell updates/sec

Title: US-09-629-719D-8
Perfect score: 61
Sequence: 1 XPRGGSVLVTC 12

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 1842

Minimum DB seq length: 0

Maximum DB seq length: 12

Post-processing: Minimum Match 0%, Maximum Match 100%

Listing first 45 summaries

Database : SPREMBL 19:*

- 1: sp_archea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phage:*
- 10: sp_plant:*
- 11: sp_rabbit:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_rvirus:*
- 16: sp_bacteriap:*
- 17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	28	45.9	11	7	077876 oreochromis
2	24	39.3	11	13	Q9PS22 xenopus lae
3	34.4	10	4	0960A7	Q969A7 homo sapien
4	21	34.4	11	4	075811 homo sapien
5	21	34.4	12	4	Q13865 homo sapien
6	21	34.4	12	4	Q96P98 homo sapien
7	19	31.1	10	4	Q9H115 homo sapien
8	19	31.1	10	4	Q9P229 homo sapien
9	18	29.5	7	11	Q63480 raiitus norvegicus
10	18	29.5	8	2	Q9R4M3 enterococcus
11	18	29.5	10	13	Q90Y93 gallus gallus
12	18	29.5	11	12	Q997C1 east affrica
13	18	29.5	12	2	Q02128 desulfobibacter
14	18	29.5	12	5	Q17140 crassostrea
15	18	29.5	12	8	Q99196 sargassum p
16	29.5	12	10	Q41856 zea mays (m)	

RESULT	1	PRELIMINARY;	PRT;	11 AA.
ID	077876			
AC	077876;			
DT	01-NOV-1998 (TREMBLEL. 08, Created)			
DT	01-NOV-1998 (TREMBLEL. 08, Last sequence update)			
DT	01-DEC-2001 (TREMBLEL. 19, Last annotation update)			
DE	MHC CLASS II B LOCUS 1 (FRAGMENT);			
OS	Oreochromis niloticus (Nile tilapia) (<i>Tilapia nilotica</i>)			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Teleostei; Buteleoste; Neoteleoste;			
OC	Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Labroidei; Cichlidae; Oreochromis.			
OC	NCBI_TATIN=8128;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE="9831513; PUBMED=9649539;			
RA	Malaga-Trillo E., Zaleska-Rutczynska Z., McAndrew B., Vincek V., Figueiroa F., Sultmann H., Klein J.;			
RT	"Linkage relationships and haplotype polymorphism among cichlid mhc class II B loci"; Genetics 149:1527-1537(1998).			
RL	Genetics 149:1527-1537(1998).			
DR	EMBL; AF049985; AAC41324.1; -.			
FT	NON_TER 1			
FT	NON_TER 1			
SQ	SEQUENCE 11 AA: 1178 MW: 9AC131FAB2D2DB45 CRC64;			

Query Match	Score	DB	Length	Best Local Similarity	Score	DB	Length	Best保守性匹配	Score	DB	Length	Best保守性匹配	Score	DB	Length	Best保守性匹配	Score	DB	Length	Best保守性匹配
Q9PS22	45.9%	oreochromis	11	71.4%	28	Q95RN9	8	homo sapien	9	Q99193	9	pseudomonas	2	Q52837	9	rhizobium 1	10	Q9UCP5	11	homo sapien
Q9PS22	45.9%	xenopus lae	13	71.4%	28	Q9XNG6	8	mus musculus	11	Q97892	11	oreochromis	4	Q46712	12	escherichia	7	Q93X21	12	zea mays (m)
Q9PS22	45.9%	homo sapien	13	71.4%	28	Q98P07	8	soil-b	12	Q9E8Q6	8	soil-b	12	Q9DSN6	8	soil-b	12	Q9E8Q5	8	soil-b
Q9PS22	45.9%	homo sapien	13	71.4%	28	Q9E8Q2	8	soil-b	12	Q9E8Q1	8	soil-b	12	Q9E8Q1	8	soil-b	12	Q9E8Q0	8	soil-b
Q9PS22	45.9%	homo sapien	13	71.4%	28	Q9E8Q3	8	soil-b	12	Q9DSN4	8	soil-b	12	Q9DSN3	8	soil-b	12	Q9DSN2	8	soil-b
Q9PS22	45.9%	homo sapien	13	71.4%	28	Q9E8Q9	8	soil-b	12	Q9E8P9	8	soil-b	12	Q9E8P8	8	soil-b	12	Q9E8P7	8	soil-b
Q9PS22	45.9%	homo sapien	13	71.4%	28	Q9E8P9	8	soil-b	12	Q9E8P8	8	soil-b	12	Q9E8P7	8	soil-b	12	Q9E8P6	8	soil-b
Q9PS22	45.9%	homo sapien	13	71.4%	28	Q9E8P7	8	soil-b	12	Q9E8P6	8	soil-b	12	Q9E8P5	8	soil-b	12	Q9E8P4	8	soil-b
Q9PS22	45.9%	homo sapien	13	71.4%	28	Q9E8P5	8	soil-b	12	Q9E8P4	8	soil-b	12	Q9E8P3	8	soil-b	12	Q9E8P2	8	soil-b
Q9PS22	45.9%	homo sapien	13	71.4%	28	Q9E8P3	8	soil-b	12	Q9E8P2	8	soil-b	12	Q9E8P1	8	soil-b	12	Q9E8P0	8	soil-b
Q9PS22	45.9%	homo sapien	13	71.4%	28	Q9E8P1	8	soil-b	12	Q9E8P0	8	soil-b	12	Q9E8P9	8	soil-b	12	Q9E8P8	8	soil-b
Q9PS22	45.9%	homo sapien	13	71.4%	28	Q9E8P0	8	soil-b	12	Q9E8P9	8	soil-b	12	Q9E8P8	8	soil-b	12	Q9E8P7	8	soil-b
Q9PS22	45.9%	homo sapien	13	71.4%	28	Q9E8P9	8	soil-b	12	Q9E8P8	8	soil-b	12	Q9E8P7	8	soil-b	12	Q9E8P6	8	soil-b
Q9PS22	45.9%	homo sapien	13	71.4%	28	Q9E8P8	8	soil-b	12	Q9E8P7	8	soil-b	12	Q9E8P6	8	soil-b	12	Q9E8P5	8	soil-b
Q9PS22	45.9%	homo sapien	13	71.4%	28	Q9E8P7	8	soil-b	12	Q9E8P6	8	soil-b	12	Q9E8P5	8	soil-b	12	Q9E8P4	8	soil-b
Q9PS22	45.9%	homo sapien	13	71.4%	28	Q9E8P6	8	soil-b	12	Q9E8P5	8	soil-b	12	Q9E8P4	8	soil-b	12	Q9E8P3	8	soil-b
Q9PS22	45.9%	homo sapien	13	71.4%	28	Q9E8P5	8	soil-b	12	Q9E8P4	8	soil-b	12	Q9E8P3	8	soil-b	12	Q9E8P2	8	soil-b
Q9PS22	45.9%	homo sapien	13	71.4%	28	Q9E8P4	8	soil-b	12	Q9E8P3	8	soil-b	12	Q9E8P2	8	soil-b	12	Q9E8P1	8	soil-b
Q9PS22	45.9%	homo sapien	13	71.4%	28	Q9E8P3	8	soil-b	12	Q9E8P2	8	soil-b	12	Q9E8P1	8	soil-b	12	Q9E8P0	8	soil-b
Q9PS22	45.9%	homo sapien	13	71.4%	28	Q9E8P2	8	soil-b	12	Q9E8P1	8	soil-b	12	Q9E8P0	8	soil-b	12	Q9E8P9	8	soil-b
Q9PS22	45.9%	homo sapien	13	71.4%	28	Q9E8P1	8	soil-b	12	Q9E8P0	8	soil-b	12	Q9E8P9	8	soil-b	12	Q9E8P8	8	soil-b
Q9PS22	45.9%	homo sapien	13	71.4%	28	Q9E8P0	8	soil-b	12	Q9E8P9	8	soil-b	12	Q9E8P8	8	soil-b	12	Q9E8P7	8	soil-b
Q9PS22	45.9%	homo sapien	13	71.4%	28	Q9E8P9	8	soil-b	12	Q9E8P8	8	soil-b	12	Q9E8P7	8	soil-b	12	Q9E8P6	8	soil-b
Q9PS22	45.9%	homo sapien	13	71.4%	28	Q9E8P8	8	soil-b	12	Q9E8P7	8	soil-b	12	Q9E8P6	8	soil-b	12	Q9E8P5	8	soil-b
Q9PS22	45.9%	homo sapien	13	71.4%	28	Q9E8P7	8	soil-b	12	Q9E8P6	8	soil-b	12	Q9E8P5	8	soil-b	12	Q9E8P4	8	soil-b
Q9PS22	45.9%	homo sapien	13	71.4%	28	Q9E8P6	8	soil-b	12	Q9E8P5	8	soil-b	12	Q9E8P4	8	soil-b	12	Q9E8P3	8	soil-b
Q9PS22	45.9%	homo sapien	13	71.4%	28	Q9E8P5	8	soil-b	12	Q9E8P4	8	soil-b	12	Q9E8P3	8	soil-b	12	Q9E8P2	8	soil-b
Q9PS22	45.9%	homo sapien	13	71.4%	28	Q9E8P4	8	soil-b	12	Q9E8P3	8	soil-b	12	Q9E8P2	8	soil-b	12	Q9E8P1	8	soil-b
Q9PS22	45.9%	homo sapien	13	71.4%	28	Q9E8P3	8	soil-b	12	Q9E8P2	8	soil-b	12	Q9E8P1	8	soil-b	12	Q9E8P0	8	soil-b
Q9PS22	45.9%	homo sapien	13	71.4%	28	Q9E8P2	8	soil-b	12	Q9E8P1	8	soil-b	12	Q9E8P0	8	soil-b	12	Q9E8P9	8	soil-b
Q9PS22	45.9%	homo sapien	13	71.4%	28	Q9E8P1	8	soil-b	12	Q9E8P0	8	soil-b	12	Q9E8P9	8	soil-b	12	Q9E8P8	8	soil-b
Q9PS22	45.9%	homo sapien	13	71.4%	28	Q9E8P0	8	soil-b	12	Q9E8P9	8	soil-b	12	Q9E8P8	8	soil-b	12	Q9E8P7	8	soil-b
Q9PS22	45.9%	homo sapien	13	71.4%	28	Q9E8P9	8	soil-b	12	Q9E8P8	8	soil-b	12	Q9E8P7	8	soil-b	12	Q9E8P6	8	soil-b
Q9PS22	45.9%	homo sapien	13	71.4%	28	Q9E8P8	8	soil-b	12	Q9E8P7	8	soil-b	12	Q9E8P6	8	soil-b	12	Q9E8P5	8	soil-b
Q9PS22	45.9%	homo sapien	13	71.4%	28	Q9E8P7	8	soil-b	12	Q9E8P6	8	soil-b	12	Q9E8P5	8	soil-b	12	Q9E8P4	8	soil-b
Q9PS22	45.9%	homo sapien	13	71.4%	28	Q9E8P6	8	soil-b	12	Q9E8P5	8	soil-b	12	Q9E8P4	8	soil-b	12	Q9E8P3	8	soil-b
Q9PS22	45.9%	homo sapien	13	71.4%	28	Q9E8P5	8	soil-b	12	Q9E8P4	8	soil-b	12	Q9E8P3	8	soil-b	12	Q9E8P2	8	soil-b
Q9PS22	45.9%	homo sapien	13	71.4%	28	Q9E8P4	8	soil-b	12	Q9E8P3	8	soil-b	12	Q9E8P2	8	soil-b	12	Q9E8P1	8	soil-b
Q9PS22	45.9%	homo sapien	13	71.4%	28	Q9E8P3	8	soil-b	12	Q9E8P2	8	soil-b	12	Q9E8P1	8	soil-b	12	Q9E8P0	8	soil-b
Q9PS22	45.9%	homo sapien	13	71.4%	28	Q9E8P2	8	soil-b	12	Q9E8P1	8	soil-b	12	Q9E8P0	8	soil-b	12	Q9E8P9	8	soil-b
Q9PS22	45.9%	homo sapien	13	71.4%	28	Q9E8P1	8	soil-b	12	Q9E8P0	8	soil-b	12	Q9E8P9	8	soil-b	12	Q9E8P8	8	soil-b
Q9PS22	45.9%	homo sapien	13	71.4%	28	Q9E8P0	8	soil-b	12	Q9E8P9	8	soil-b	12	Q9E8P8	8					

AC	Q9PS22;	PRELIMINARY;	PRT;	11 AA.
DT	01-MAY-2000 (TREMBLrel. 13, Created)			
DT	01-MAY-2000 (TREMBLrel. 13, Last sequence update)			
DT	01-JUN-2001 (TREMBLrel. 17, Last annotation update)			
DE	HYDRIN 1', VASOTOCINYL-GLY-LYS.			
OS	Xenopus laevis (African clawed frog).			
OC	Eutaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;			
OC	Xenopodinae; Xenopus.			
NCBI_TAXID	8355;			
RN	[1]			
RP	SEQUENCE.			
RX	MEDLINE=93200145; PubMed=8452872;			
RA	Iwanuro S., Hayashi H., Kikuyama S.;			
RT	"An additional arginine-vasotocin-related peptide, vasotocinyl-Gly-Lys, in Xenopus neurohypophysis."			
RT	Biochim. Biophys. Acta 1176:143-147(1993).			
InterPro	IPR000981: Neurhypophysis-horm.			
DR	Pfam: PF00220; hormone_1.			
PROSITE	PS00264; NEUROPOPHYS_HORM; 1.			
DR	SEQUENCE: PS00264; 11 AA; 1238 MW; CC5B57EB176EB456 CRC64;			
Qy	Query Match	39.3%; Score 24; DB 13; Length 11; Best Local Similarity 100.0%; Pred. No. 9.8e+02; Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
Db	2 PRGG 5 : 7 PRGG 10			
RESULT	3			
ID	Q960A7	PRELIMINARY;	PRT;	10 AA.
AC	Q960A7;			
DT	01-DEC-2001 (TREMBLrel. 19, Created)			
DT	01-DEC-2001 (TREMBLrel. 19, Last sequence update)			
DT	01-DEC-2001 (TREMBLrel. 19, Last annotation update)			
DE	BA151A2.1 (CDG42 GUARINE EXCHANGE FACTOR (GEF) 9 (COLLYBISTIN, PEM-2, HPEM-2, KIAA0424)) (FRAGMENT).			
GN	ARIGE99.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
NCBI_TAXID	9606;			
[1]	SEQUENCE FROM N.A.			
RP	WHITEHEAD S.; Submitted (SEB-2001) to the EMBL/GenBank/DDBJ databases.			
DR	EMBL; AL451105; CAC88408.1; -.			
RL	NON-TER 10			
FT	SEQUENCE 10 AA; 1122 MW; 39925CB878640043 CRC64;			
SQ				
Qy	Query Match	34.4%; Score 21; DB 4; Length 10; Best Local Similarity 100.0%; Pred. No. 2.9e+03; Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
Db	3 RGGS 6 : 5 RGGS 8			
RESULT	6			
ID	Q96998	PRELIMINARY;	PRT;	12 AA.
AC	Q96P98			
DT	01-DEC-2001 (TREMBLrel. 19, Created)			
DT	01-DEC-2001 (TREMBLrel. 19, Last sequence update)			
DT	01-DEC-2001 (TREMBLrel. 19, Last annotation update)			
DE	CD27-BINDING PROTEIN (FRAGMENT).			
OS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
NCBI_TAXID	8355;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	TISSUE-OVARIAN CARCINOMA;			
RA	MEDLINE=8834547; PubMed=9681822;			
RA	LEE H., MAHLE N.J.			
RT	"Isolation and characterization of four alternate c-erbB3 transcripts expressed in ovarian carcinoma-derived cell lines and normal human tissues."			
RT	Oncogene 16:3243-3252(1998).			
RL	EMBL; U88358; AAC39858.1; -.			
DR	NON-TER 11 AA; 1017 MW; 21B236366BB72878 CRC64;			
FT	SEQUENCE 11 AA; 1017 MW; 21B236366BB72878 CRC64;			
SQ				
Qy	Query Match	34.4%; Score 21; DB 4; Length 11; Best Local Similarity 100.0%; Pred. No. 3.2e+03; Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;		
Db	2 PRGG 5 : 8 PKGG 11			
RESULT	5			
ID	Q13865	PRELIMINARY;	PRT;	12 AA.
AC	Q13865;			
DT	01-NOV-1996 (TREMBLrel. 01, Created)			
DT	01-NOV-1996 (TREMBLrel. 01, Last sequence update)			
DT	01-DEC-2001 (TREMBLrel. 19, Last annotation update)			
DE	KINESIN LIGHT CHAIN.			
GN	BETA-KINESIN.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
NCBI_TAXID	9606;			
[1]	SEQUENCE FROM N.A.			
RP	TISSUE-PLACENTA;			
RC	MEDLINE=9101110; PubMed=8945637;			
RA	CHERNAJOWSKY Y., BROWN A., JONES T.A.;			
RT	"Promoter first exon/intron characterization and chromosomal location of the human light chain (beta) kinesin gene."			
RT	DNA Cell Biol. 15:965-974(1996).			
RL	EMBL; X69658; CAA49349.1; -.			
DR	SEQUENCE 12 AA; 1274 MW; 3FBBD34EE165A5B8 CRC64;			
SQ				
Qy	Query Match	34.4%; Score 21; DB 4; Length 12; Best Local Similarity 100.0%; Pred. No. 3.5e+03; Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
Db	3 RGGS 6 : 3 RGGS 6			
RESULT	6			
ID	Q96998	PRELIMINARY;	PRT;	12 AA.
AC	Q96P98			
DT	01-DEC-2001 (TREMBLrel. 19, Created)			
DT	01-DEC-2001 (TREMBLrel. 19, Last sequence update)			
DT	01-DEC-2001 (TREMBLrel. 19, Last annotation update)			
DE	CD27-BINDING PROTEIN (FRAGMENT).			
OS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
NCBI_TAXID	8355;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	C-EERBB-3.			
RA	Homo sapiens (Human).			
RT	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
NCBI_TAXID	9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	TISSUE-OVARIAN CARCINOMA;			
RA	MEDLINE=8834547; PubMed=9681822;			
RA	LEE H., MAHLE N.J.			
RT	"Isolation and characterization of four alternate c-erbB3 transcripts expressed in ovarian carcinoma-derived cell lines and normal human tissues."			
RT	Oncogene 16:3243-3252(1998).			
RL	EMBL; U88358; AAC39858.1; -.			
DR	NON-TER 11 AA; 1017 MW; 21B236366BB72878 CRC64;			
FT	SEQUENCE 11 AA; 1017 MW; 21B236366BB72878 CRC64;			
SQ				
Qy	Query Match	34.4%; Score 21; DB 4; Length 11; Best Local Similarity 100.0%; Pred. No. 3.2e+03; Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;		
Db	2 PRGG 5 : 8 PKGG 11			
RESULT	5			
ID	Q13865	PRELIMINARY;	PRT;	12 AA.
AC	Q13865;			
DT	01-NOV-1996 (TREMBLrel. 01, Created)			
DT	01-NOV-1996 (TREMBLrel. 01, Last sequence update)			
DT	01-DEC-2001 (TREMBLrel. 19, Last annotation update)			
DE	KINESIN LIGHT CHAIN.			
GN	BETA-KINESIN.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
NCBI_TAXID	9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	C-EERBB-3.			
RA	Homo sapiens (Human).			
RT	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
NCBI_TAXID	9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	C-EERBB-3.			
RA	Homo sapiens (Human).			
RT	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
NCBI_TAXID	9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	C-EERBB-3.			
RA	Homo sapiens (Human).			
RT	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
NCBI_TAXID	9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	C-EERBB-3.			
RA	Homo sapiens (Human).			
RT	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
NCBI_TAXID	9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	C-EERBB-3.			
RA	Homo sapiens (Human).			
RT	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
NCBI_TAXID	9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	C-EERBB-3.			
RA	Homo sapiens (Human).			
RT	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
NCBI_TAXID	9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	C-EERBB-3.			
RA	Homo sapiens (Human).			
RT	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
NCBI_TAXID	9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	C-EERBB-3.			
RA	Homo sapiens (Human).			
RT	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
NCBI_TAXID	9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	C-EERBB-3.			
RA	Homo sapiens (Human).			
RT	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
NCBI_TAXID	9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	C-EERBB-3.			
RA	Homo sapiens (Human).			
RT	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
NCBI_TAXID	9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	C-EERBB-3.			
RA	Homo sapiens (Human).			
RT	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
NCBI_TAXID	9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	C-EERBB-3.			
RA	Homo sapiens (Human).			
RT	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
NCBI_TAXID	9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	C-EERBB-3.			
RA	Homo sapiens (Human).			
RT	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
NCBI_TAXID	9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	C-EERBB-3.			
RA	Homo sapiens (Human).			
RT	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
NCBI_TAXID	9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	C-EERBB-3.			
RA	Homo sapiens (Human).			
RT	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
NCBI_TAXID	9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	C-EERBB-3.			
RA	Homo sapiens (Human).			
RT	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
NCBI_TAXID	9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	C-EERBB-3.			
RA	Homo sapiens (Human).			
RT	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
NCBI_TAXID	9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	C-EERBB-3.			
RA	Homo sapiens (Human).			
RT	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
NCBI_TAXID	9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	C-EERBB-3.			
RA	Homo sapiens (Human).			
RT	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
NCBI_TAXID	9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	C-EERBB-3.			
RA	Homo sapiens (Human).			
RT	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
NCBI_TAXID	9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	C-EERBB-3.			
RA	Homo sapiens (Human).			
RT	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
NCBI_TAXID	9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	C-EERBB-3.			
RA	Homo sapiens (Human).			
RT	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
NCBI_TAXID	9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	C-EERBB-3.			
RA	Homo sapiens (Human).			
RT	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
NCBI_TAXID	9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	C-EERBB-3.			
RA	Homo sapiens (Human).			
RT	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
NCBI_TAXID	9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	C-EERBB-3.			
RA	Homo sapiens (Human).			
RT	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
NCBI_TAXID	9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	C-EERBB-3.			
RA	Homo sapiens (Human).			
RT	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
NCBI_TAXID	9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	C-EERBB-3.			
RA	Homo sapiens (Human).			
RT	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
NCBI_TAX				

OX	NCBI_TAXID=9606;	RT	effects of type II mutation on receptor function.";
RN	[1]	RL	Biochem. Biophys. Res. Commun. 178:1413-1420(1991).
SEQUENCE FROM N.A.		DR	EMBL; S51343; AAB19485. 2; -.
RA	Kang H.S., Park Y.J., Jung H.M., Jun D.Y., Huh T.L., Kim Y.H.;	KW	Receptor.
RT	"Characterization of TPA-responsive genes in U937 cells using ordered	FT	NON_TER
RL	differential display PCR";	FT	1 10
DR	Submitted (JUL-2001) to the EMBL/GenBank/DDJB databases.	FT	NON_TER 10 AA; 10 MW;
EMBL; AF401214; AAL02171.1; -.		SQ	439DEEAEB87B1727 CRC64;
FT		SEQUENCE	12 AA; 1333 MW; 977A27103ADER5A1 CRC64;
SQ		Query Match	34.4%; Score 21; DB 4; Length 12;
Best Local Similarity	66.7%; Pred. No. 3.5e+03;	Matches	Pred. No. 6.4e+03;
Matches	4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;	Qy	Score 19; DB 4; Length 10;
Db	2 VLVTGC 7	Qy	31.1%; Score 19; DB 4; Length 10;
RESULT	7	Best Local Similarity	60.0%; Pred. No. 6.4e+03;
ID	O9H15	Matches	1; Mismatches 1; Indels 0; Gaps 0;
PRELIMINARY;	PRT; 10 AA.	Qy	8 VLVTGC 12
ID	O9H15	Db	3 LLEGC 7
AC	09H15	RESULT	9
DT	01-MAR-2001 (TREMBLrel. 16, Created)	ID	063480
DT	01-MAR-2001 (TREMBLrel. 16, Last sequence update)	PRELIMINARY;	PRT; 7 AA.
DT	01-MAR-2001 (TREMBLrel. 16, Last annotation update)	ID	063480
DE	MUTANT_BETA-GLOBIN (FRAGMENT).	AC	063480
DE	HBB.	DT	01-NOV-1996 (TREMBLrel. 01, Last sequence update)
GN	Homo sapiens (Human).	DT	01-DEC-2001 (TREMBLrel. 19, Last annotation update)
OS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	DE	TR4-NS ORPHAN RECEPTOR (FRAGMENT).
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.	OS	Rattus norvegicus (Rat).
OX	NCBI_TaxID=9606;	OC	Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
RN	[1]	OX	Rattus; Muridae; Murinae; Rattus.
SEQUENCE FROM N.A.		RN	NCBI_TaxID=10116;
RA	Yang Z., Chu J., Ban G., Shi L., Huang X., Lin K., Tao Y.;	RP	SEQUENCE FROM N.A.
RT	"Molecular characterization of beta thalassemia in Yunnan, China.";	RX	MEDLINE=96198747; PubMed=8612486;
RL	Submitted (NOV-2000) to the EMBL/GenBank/DDJB databases.	RA	Yoshikawa T., Makino S., Gao X.M., Xing G.Q., Chuang D.M.,
DR	EMBL; AY013300; AAC46183.1; -.	DE	Detera-Wadleigh S.D.;
FT	NON_TER 1	RT	"Splice variants of rat TR4 orphan receptor: differential expression
FT	NON_TER 10	RT	of novel sequences in the 5'-untranslated region and C-terminal
SQ	SEQUENCE 10 AA; 1042 MW; 2210B242C73C448 CRC64;	RL	domain"; Endocrinology 137:1562-1571(1996).
RESULT	8	DR	EMBL; U59125; AAB02827.1; -.
Q9P2Z9	PRELIMINARY; PRT; 10 AA.	KW	Receptor.
ID	Q9P2Z9	FT	NON_TER 1 1 1
AC	Q9P2Z9;	SEQUENCE	7 AA; 758 MW; 672AA87864005350 CRC64;
DR	01-OCT-2000 (TREMBLrel. 15, Created)	Query Match	29.5%; Score 18; DB 11; Length 7;
DT	01-OCT-2000 (TREMBLrel. 15, Last sequence update)	Best Local Similarity	60.0%; Pred. No. 5.6e+05;
DT	01-OCT-2000 (TREMBLrel. 15, Last annotation update)	Matches	1; Mismatches 1; Indels 0; Gaps 0;
DE	EPIDERMAL GROWTH FACTOR RECEPTOR (FRAGMENT).	Qy	3 RGGSV 7
OS	Homo sapiens (Human).	Db	3 RGGDL 7
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	RESULT	10
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	ID	O9R4M3
OC	NCBITaxID=9606;	PRELIMINARY;	PRT; 8 AA.
OX	[1]	ID	O9R4M3
RP	SEQUENCE FROM N.A.	AC	O9R4M3;
RX	MEDLINE=9137091; PubMed=1678600;	DT	01-MAY-2000 (TREMBLrel. 13, Last sequence update)
RA	Humphrey P.A., Gangarosa L.M., Wong A.J., Archer G.E.,	DT	01-MAY-2000 (TREMBLrel. 13, Last annotation update)
RA	Lund-Johansen M., Bjerkvig R., Laerum O.D., Friedman H.S.,	DE	COB1=BACTERIAL SEX PHEROMONE.
RA	Bigner D.D.;	OS	Enterococcus faecalis (Streptococcus faecalis).
RT	"Deletion-mutant epidermal growth factor receptor in human gliomas:	OC	Bacteria; Firmicutes; Bacillus/Clostridium group; Enterococcaceae;
OX	NCBI_TAXID=1351;	OX	Enterococcus.
RN	[1]	RN	NCBI_TAXID=1351;
SEQUENCE		RP	SEQUENCE.
RX	MEDLINE=95290767; PubMed=7772836;	RA	Nakayama J., Abe Y., Ono Y., Isogai A., Suzuki A.;
RA	Lund-Johansen M., Bjerkvig R., Laerum O.D., Friedman H.S.,	RT	"Isolation and structure of the Enterococcus faecalis sex pheromone,
RA	Bigner D.D.;	RT	COB1, that induces conjugal transfer of the hemolysin/bacteriocin

QY	6	SVLTGT	11	Query Match Best Local Similarity 66.7%; Pred. No. 5.6e+05; Mismatches 1; Indels 0; Gaps 0;	Score 18; DB 2; Length 8; Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;	RT plasmids, pOB1 and pY11.;" RL Biosci. Biotechnol. Biochem. 59:703-705(1995).; SQ SEQUENCE 8 AA; 741 MW; 83D8773C73CDC2 CRC64;
Db	2	AYLVLG	7			
RESULT	11			Query Match Best Local Similarity 29.5%; Score 18; DB 12; Length 11; Matches 2; Conservative 4; Mismatches 2; Indels 0; Gaps 0;	Score 18; DB 12; Length 11; Matches 2; Conservative 4; Mismatches 2; Indels 0; Gaps 0;	
ID	Q90Y93	PRELIMINARY;	PRT;	RT 01-DEC-2001 (TREMBLrel. 19, Created) 01-DEC-2001 (TREMBLrel. 19, Last sequence update)	RT 01-NOV-1996 (TREMBLrel. 01, Created) 01-MAY-1999 (TREMBLrel. 10, Last sequence update)	RT 01-MAY-1999 (TREMBLrel. 10, Last annotation update)
QY	6	SVLTGT	11	ID Q90Y93;	ID Q90Y93;	DE HYPOTHEtical PROTEin IN HYDA 5'REGION (FRAGMENT).
Db	2	AYLVLG	7	DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)	OS Desulfovibrio vulgaris (strain Hildenborough).	OS Desulfovibrio vulgaris (strain Hildenborough).
GN	GH			DE Bacteria; Proteobacteria; delta subdivision; Desulfovibrio.	OC	OC
OS	Galus galus (Chicken).			RA Van den Berg W.A.M.; Stokkermans J.P.W.G., Van Dongen W.M.A.M.; "The operon for the Fe-hydrogenase in Desulfovibrio vulgaris (Hildenborough); mapping of the transcript and regulation of expression.";	RA Van den Berg W.A.M.; Stokkermans J.P.W.G., Van Dongen W.M.A.M.; "The operon for the Fe-hydrogenase in Desulfovibrio vulgaris (Hildenborough); mapping of the transcript and regulation of expression.";	RA Van den Berg W.A.M.; Stokkermans J.P.W.G., Van Dongen W.M.A.M.; "The operon for the Fe-hydrogenase in Desulfovibrio vulgaris (Hildenborough); mapping of the transcript and regulation of expression.";
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauromorphia; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.			RT MEDLINE:93307640; PubMed:7686524;	RT MEDLINE:93307640; PubMed:7686524;	RT MEDLINE:93307640; PubMed:7686524;
OC	[1]			RP SEQUENCE FROM N.A.	RP SEQUENCE FROM N.A.	RP SEQUENCE FROM N.A.
RN	NCBI_TAXID:9031;			RA [1]	RA [1]	RA [1]
RP	SEQUENCE FROM N.A.			RT FEMS Microbiol. Lett. 110:85-90(1993).	RT FEMS Microbiol. Lett. 110:85-90(1993).	RT FEMS Microbiol. Lett. 110:85-90(1993).
RA	Kansaku N., Nakada A., Yagi E., Okabayashi H., Guemeze D.; RT "Genetic variation of chicken growth hormone gene.";			RA RX MEDLINE:93203856; PubMed:3888621;	RA RX MEDLINE:93203856; PubMed:3888621;	RA RX MEDLINE:93203856; PubMed:3888621;
RT	Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.			RA RA Vooroudou G., Brenner S.; "Nucleotide sequence of the gene encoding the hydrogenase from Desulfovibrio vulgaris (Hildenborough)." ;	RA RA Vooroudou G., Brenner S.; "Nucleotide sequence of the gene encoding the hydrogenase from Desulfovibrio vulgaris (Hildenborough)." ;	RA RA Vooroudou G., Brenner S.; "Nucleotide sequence of the gene encoding the hydrogenase from Desulfovibrio vulgaris (Hildenborough)." ;
DR	EMBL: AB061722; BAB69037.1; -			RT RT Desulfovibrio vulgaris (Hildenborough).";	RT RT Desulfovibrio vulgaris (Hildenborough).";	RT RT Desulfovibrio vulgaris (Hildenborough).";
FT	NON_TER 1			RT RL Eur. J. Biochem. 148:515-520(1985).	RT RL Eur. J. Biochem. 148:515-520(1985).	RT RL Eur. J. Biochem. 148:515-520(1985).
FT	NON_TER 10			RN RN [3]	RN RN [3]	RN RN [3]
SQ	SEQUENCE 10 AA; 1155 MW; 6841751775A40AB CRC64;			RP REVISIOnS.	RP REVISIOnS.	RP REVISIOnS.
QY	2	PRG	4	RA Van den Berg W.A.M.;	RA Van den Berg W.A.M.;	RA Van den Berg W.A.M.;
Db	7	PRG	9	RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.	RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.	RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
RESULT	12			RT EMBL: Z15142; CAB37617.1; -	RT EMBL: Z15142; CAB37617.1; -	RT EMBL: Z15142; CAB37617.1; -
Q997C1	PRELIMINARY;	PRT;	11 AA.	KW Hypothetical protein.	KW Hypothetical protein.	KW Hypothetical protein.
ID	Q997C1			FT NON_TER 1	FT NON_TER 1	FT NON_TER 1
AC	Q997C1;			SQ SEQUENCE 12 AA; 1261 MW; C831123540BAAGCD CRC64;	SQ SEQUENCE 12 AA; 1261 MW; C831123540BAAGCD CRC64;	SQ SEQUENCE 12 AA; 1261 MW; C831123540BAAGCD CRC64;
DT	01-JUN-2001 (TREMBLrel. 17, Last sequence update)			RP REVISIOnS.	RP REVISIOnS.	RP REVISIOnS.
DT	01-JUN-2001 (TREMBLrel. 17, Last annotation update)			RA Van den Berg W.A.M.;	RA Van den Berg W.A.M.;	RA Van den Berg W.A.M.;
DE	COT PROTEIN (FRAGMENT).			RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.	RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.	RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
OS	East African cassava mosaic virus.			RT EMBL: Z15142; CAB37617.1; -	RT EMBL: Z15142; CAB37617.1; -	RT EMBL: Z15142; CAB37617.1; -
OC	VIRUSES; ssDNA viruses; Geminiviridae; Begomovirus.			RT EUR. J. BIOCHEM. 148:515-520(1985).	RT EUR. J. BIOCHEM. 148:515-520(1985).	RT EUR. J. BIOCHEM. 148:515-520(1985).
OX	NBIL_TAXID:62079;			RT EUR. J. BIOCHEM. 148:515-520(1985).	RT EUR. J. BIOCHEM. 148:515-520(1985).	RT EUR. J. BIOCHEM. 148:515-520(1985).
[1]	SEQUENCE FROM N.A.			RT EUR. J. BIOCHEM. 148:515-520(1985).	RT EUR. J. BIOCHEM. 148:515-520(1985).	RT EUR. J. BIOCHEM. 148:515-520(1985).
RNA	MEDLINE:21103006; PubMed:11172108;			RT EUR. J. BIOCHEM. 148:515-520(1985).	RT EUR. J. BIOCHEM. 148:515-520(1985).	RT EUR. J. BIOCHEM. 148:515-520(1985).
RP	Pita J.S., Fondong V.N., Sangare A., Otim-Nape G.W., Ogwal S.,			RT EUR. J. BIOCHEM. 148:515-520(1985).	RT EUR. J. BIOCHEM. 148:515-520(1985).	RT EUR. J. BIOCHEM. 148:515-520(1985).
RA	Fauquet C.M.;			RT EUR. J. BIOCHEM. 148:515-520(1985).	RT EUR. J. BIOCHEM. 148:515-520(1985).	RT EUR. J. BIOCHEM. 148:515-520(1985).
RA	"Recombination, pseudorecombination and synergism of geminiviruses are determinant keys to the epidemic of severe cassava mosaic disease in			RT EUR. J. BIOCHEM. 148:515-520(1985).	RT EUR. J. BIOCHEM. 148:515-520(1985).	RT EUR. J. BIOCHEM. 148:515-520(1985).
RT	Uganda.",			RT EUR. J. BIOCHEM. 148:515-520(1985).	RT EUR. J. BIOCHEM. 148:515-520(1985).	RT EUR. J. BIOCHEM. 148:515-520(1985).
RT	J. Gen. Virol. 82:655-665(2001).			RT EUR. J. BIOCHEM. 148:515-520(1985).	RT EUR. J. BIOCHEM. 148:515-520(1985).	RT EUR. J. BIOCHEM. 148:515-520(1985).
DR	AF230374; AAK26738.1; -			RT EUR. J. BIOCHEM. 148:515-520(1985).	RT EUR. J. BIOCHEM. 148:515-520(1985).	RT EUR. J. BIOCHEM. 148:515-520(1985).
FT	NON_TER 11			RT EUR. J. BIOCHEM. 148:515-520(1985).	RT EUR. J. BIOCHEM. 148:515-520(1985).	RT EUR. J. BIOCHEM. 148:515-520(1985).
SQ	SEQUENCE 11 AA; 1216 MW; 7751D0695AA86774 CRC64;			RT EUR. J. BIOCHEM. 148:515-520(1985).	RT EUR. J. BIOCHEM. 148:515-520(1985).	RT EUR. J. BIOCHEM. 148:515-520(1985).
RESULT	13			RT EUR. J. BIOCHEM. 148:515-520(1985).	RT EUR. J. BIOCHEM. 148:515-520(1985).	RT EUR. J. BIOCHEM. 148:515-520(1985).
QY	3	RGGSVLVT	10	Query Match Best Local Similarity 29.5%; Score 18; DB 12; Length 11; Matches 2; Conservative 4; Mismatches 2; Indels 0; Gaps 0;	Query Match Best Local Similarity 29.5%; Score 18; DB 12; Length 11; Matches 2; Conservative 4; Mismatches 2; Indels 0; Gaps 0;	Query Match Best Local Similarity 29.5%; Score 18; DB 12; Length 11; Matches 2; Conservative 4; Mismatches 2; Indels 0; Gaps 0;
Db	4	RPGDIIS	11	RT EUR. J. BIOCHEM. 148:515-520(1985).	RT EUR. J. BIOCHEM. 148:515-520(1985).	RT EUR. J. BIOCHEM. 148:515-520(1985).
RESULT	14			RT EUR. J. BIOCHEM. 148:515-520(1985).	RT EUR. J. BIOCHEM. 148:515-520(1985).	RT EUR. J. BIOCHEM. 148:515-520(1985).
ID	Q17140	PRELIMINARY;	PRT;	RT EUR. J. BIOCHEM. 148:515-520(1985).	RT EUR. J. BIOCHEM. 148:515-520(1985).	RT EUR. J. BIOCHEM. 148:515-520(1985).
AC	Q17140;			RT EUR. J. BIOCHEM. 148:515-520(1985).	RT EUR. J. BIOCHEM. 148:515-520(1985).	RT EUR. J. BIOCHEM. 148:515-520(1985).
DT	01-JAN-1998 (TREMBLrel. 05, Created)			RT EUR. J. BIOCHEM. 148:515-520(1985).	RT EUR. J. BIOCHEM. 148:515-520(1985).	RT EUR. J. BIOCHEM. 148:515-520(1985).
DT	01-JAN-1998 (TREMBLrel. 05, Last sequence update)			RT EUR. J. BIOCHEM. 148:515-520(1985).	RT EUR. J. BIOCHEM. 148:515-520(1985).	RT EUR. J. BIOCHEM. 148:515-520(1985).
DE	PUTATIVE C-MYC HOMOLOG (FRAGMENT).			RT EUR. J. BIOCHEM. 148:515-520(1985).	RT EUR. J. BIOCHEM. 148:515-520(1985).	RT EUR. J. BIOCHEM. 148:515-520(1985).
OS	Croissostrea virginica (Eastern oyster)			RT EUR. J. BIOCHEM. 148:515-520(1985).	RT EUR. J. BIOCHEM. 148:515-520(1985).	RT EUR. J. BIOCHEM. 148:515-520(1985).
OC	Bivalvia; Mollusca; Bivalvia; Pteriomorphia; Ostreoida;			RT EUR. J. BIOCHEM. 148:515-520(1985).	RT EUR. J. BIOCHEM. 148:515-520(1985).	RT EUR. J. BIOCHEM. 148:515-520(1985).
OC	Ostrea; Ostreidae; Crassostrea.			RT EUR. J. BIOCHEM. 148:515-520(1985).	RT EUR. J. BIOCHEM. 148:515-520(1985).	RT EUR. J. BIOCHEM. 148:515-520(1985).
NCBI_TAXID:6565;				RT EUR. J. BIOCHEM. 148:515-520(1985).	RT EUR. J. BIOCHEM. 148:515-520(1985).	RT EUR. J. BIOCHEM. 148:515-520(1985).
[1]	SEQUENCE FROM N.A.			RT EUR. J. BIOCHEM. 148:515-520(1985).	RT EUR. J. BIOCHEM. 148:515-520(1985).	RT EUR. J. BIOCHEM. 148:515-520(1985).
RP	SEQUENCE FROM N.A.			RT EUR. J. BIOCHEM. 148:515-520(1985).	RT EUR. J. BIOCHEM. 148:515-520(1985).	RT EUR. J. BIOCHEM. 148:515-520(1985).
RC	STRAIN=WESTERN NORTH ATLANTIC WILD OYSTER;			RT EUR. J. BIOCHEM. 148:515-520(1985).	RT EUR. J. BIOCHEM. 148:515-520(1985).	RT EUR. J. BIOCHEM. 148:515-520(1985).
RA	Hare M.P., Ayotte J.C.;			RT EUR. J. BIOCHEM. 148:515-520(1985).	RT EUR. J. BIOCHEM. 148:515-520(1985).	RT EUR. J. BIOCHEM. 148:515-520(1985).
RT	"Population Structure in the American Oyster as Inferred by Nuclear Gene Genealogies".			RT EUR. J. BIOCHEM. 148:515-520(1985).	RT EUR. J. BIOCHEM. 148:515-520(1985).	RT EUR. J. BIOCHEM. 148:515-520(1985).
RL	MOL. BIOL. EVOL. 0:0-0(1997).			RT EUR. J. BIOCHEM. 148:515-520(1985).	RT EUR. J. BIOCHEM. 148:515-520(1985).	RT EUR. J. BIOCHEM. 148:515-520(1985).

DR EMBL; AAF024522; AAB82269.1; ~.
 FT 1
 NON_TER 1
 FT 12 12 MW; FF6312ABFE1775AA CRC64;
 SQ SEQUENCE 12 AA; 1334 MW; FF6312ABFE1775AA CRC64;

Query Match 29.5%; Score 18; DB 5; Length 12;
 Best Local Similarity 100.0%; Pred. No. 1.1e+04;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 2 PRG 4
 Db 7 PRG 9

RESULT 15

Q9GI96 PRELIMINARY; PRT; 12 AA.

ID Q9GI96 AC 09G196; DT 01-MAR-2001 (TREMBrel. 16, Created)
 DT 01-MAR-2001 (TREMBrel. 16, Last sequence update)

DE RIBULOSE-1,5-BISPHOSPHATE CARBOXYLASE/OXYGENASE SMALL SUBUNIT (FRAGMENT).

GN RBCS.

OS Sargassum polycystum.

OG Chloroplast.

OC Eukaryota; stramenopiles; Phaeophyceae; Fucales; Sargassaceae;

OC Sargassum. NCBI_TaxID=127578;

RN [1]

RP SQUENCE FROM N.A.

RC STRAIN=NEP127;

RA Phillips N.E.; RT "Molecular phylogenetic analysis of the pan-pacific genus *Sargassum* (Fucales, Phaeophyceae)."; RL Thesis (1998), University of Hawaii.

RN [2]

RP SQUENCE FROM N.A.

RC STRAIN=NEP127;

RA Phillips N.E., Smith C.M., Morden C.W.; RT "Testing the systematics of the genus *Sargassum* (Fucales, Phaeophyceae) with the Rubisco operon.;" RL Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases. DR EMBL; AAF244344; AAF98114.1; ~.
 KW Chloroplast.

FT NON_TER 12 SQ SEQUENCE 12 AA; 1379 MW; 373D121250CERB867 CRC64;

Query Match 29.5%; Score 18; DB 8; Length 12;
 Best Local Similarity 60.0%; Pred. No. 1.1e+04;
 Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 Qy 8 LTPGC 12
 Db 3 LTPGC 7

Search completed: October 10, 2002, 06:23:38
 Job time: 389 sec

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OM protein - protein search, using sw model

Run on: October 10, 2002, 06:16:24 ; Search time 47.09 Seconds
(without alignments)

Scoring table: BLOSUM62

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 158732

Min DB seq length: 0

Max DB seq length: 12

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_032802:*

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22: /SIDS1/gcadata/geneseq/geneseq -emb1/AA2001.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	Score	% Match	Query Length	DB ID	Description	Location/Qualifiers	Notes
1	51	83.6	11	16	AAR80118	ICAM CD54 (38-48)	
2	45	73.8	12	16	AAR80117	ICAM CD54 (37-48)	
3	45	73.8	12	16	AAR80116	ICAM CD54 (37-48)	
4	45	73.8	12	18	AARW4098	ICAM-1 beta subunit	
5	45	73.8	12	18	AARW4101	ICAM-1 beta subunit	
6	30	49.2	11	20	AAW83406	Human thioredoxin	
7	45.9	5	10	20	AAP80452	Sequence of part o	
8	28	45.9	5	19	AAW70875	ICAM-1 peptide fra	
9	28	45.9	6	14	AAR8037	Peptide which bind	
10	28	45.9	6	14	AAR84089	Peptide which bind	
11	28	45.9	7	18	AAW34379	PKB substrate #26.	

ALIGNMENTS

12	28	45.9	7	21	AYEG3234	Protocadherin cell
13	28	45.9	8	21	AYEG3237	Protocadherin cell
14	28	45.9	9	21	AYEG3240	Protocadherin cell
15	28	45.9	10	21	AYEG3243	Protocadherin cell
16	28	45.9	10	22	AAG36705	Human complementar
17	28	45.9	10	22	AAG96811	Human complementar
18	28	45.9	10	22	AAG96815	Human complementar
19	28	45.9	11	21	AYEG3246	Protocadherin cell
20	27	44.3	6	14	AAR34098	Antigen to generat
21	27	44.3	6	14	AAR34036	Antigen to generat
22	27	44.3	6	14	AAR34088	Antigen to generat
23	27	44.3	10	19	AAY87507	Molecular mimetic
24	27	44.3	12	21	AAY4514	Human CD4 protein
25	26	42.6	9	11	AAG83955	Cyclic cell adhesi
26	26	42.6	9	14	AAR31421	Cyclic platelet ag
27	26	42.6	9	21	AAB09405	Hepatitis GB virus
28	26	42.6	10	21	AAY87210	Human secreted pro
29	25	41.0	10	22	AAE06187	Human gene 58 enco
30	26	42.6	10	22	AAG85747	Saccharomyces cere
31	26	42.6	10	22	AAG88108	Saccharomyces cere
32	25	41.0	10	16	AAY4919	Human presenilin I
33	25	41.0	10	20	AAY6180	Urea plasminogen a
34	25	41.0	10	21	AAB0156	scrv 9A4 clone 4H
35	25	41.0	10	22	AAM50194	Plasmid PBS24aben
36	25	41.0	10	22	AAB8572	Monoclonal antibod
37	25	41.0	10	22	AAB85872	Saccharomyces cere
38	25	41.0	10	22	AAB72784	Antibacterial pept
39	25	41.0	10	22	AAB72785	D. teissieri IMD pe
40	25	41.0	10	22	AAB57730	Rheumatoid arthr
41	25	41.0	11	20	AAY2019	Partial sequence o
42	25	41.0	12	10	AAP91137	Partial sequence o
43	25	41.0	12	10	AAP91134	Urokinase peptid
44	25	41.0	12	16	AAB72784	Peptide which bind
45	24	39.3	5	14	AAR34099	

XX
 PT Changing peptide reactivity via conjugation with a second peptide -
 PT causes change in conformation of first peptide, pref. LFA-1 and
 XX ICAM-1 functional domain derived peptide(s)
 PS Claim 30; Page 42; 64pp; English.
 XX
 CC Synthetic sub sequences of ICAM-1 CD54 (AAR80113-24), LFA-1 beta CD18
 CC (AAR80109) or LFA-1 alpha CD18 (AAR80111-12) are used to block
 CC ICAM/LFA binding interaction by binding to a target protein in a
 CC manner that precludes the normal binding reaction between ICAM-1 and
 CC LFA-1. Alternatively, the peptide induces a conformational change
 CC in the target protein, enhancing the reactivity of a second
 CC peptide. The peptides have immunosuppressive appln.
 XX
 SQ Sequence 11 AA;
 Query Match 83.6%; Score 51; DB 16; Length 11;
 St Local Similarity 100.0%; Pred. No. 0.052; Mismatches 0; Indels 0; Gaps 0;
 Res 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 PRGGSVLVTG 11
 |||||||
 Db 2 prggsvlvtg 11
 RESULT 2
 AAR80117
 AAR80117 standard; Peptide: 12 AA.
 XX
 AC AAR80117;
 XX
 DT 05-MAR-1996 (first entry)
 DE ICAM CD54 (37-48) cyclic peptide RB-1-51.
 DE ICAM CD54 (37-48) cyclic peptide RB-1-51.
 KW ICAM-1; CD54; intercellular adhesion molecule-1; integrin; LFA-1;
 KW leucocyte function-associated antigen; immunosuppressive;
 KW RB-1-51; cyclic.
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 1
 /note= "Ile at position 37 of CD54 is Cys
 at position 1 of RB-1-51"
 FT Disulfide-bond 1..12
 /note= "cysteine-cysteine disulfide bond"
 PN WO9528170-A1.
 PD 26-OCT-1995.
 PR 19-APR-1995; 95WO-US04886.
 PA (UNIV) UNIV KANSAS.
 PI Benedict S, Chan MA, Slahaan TJ, Tibbets SA,
 XX DR WPI; 1995-373631/48.
 XX
 PT Changing peptide reactivity via conjugation with a second peptide -
 PT causes change in conformation of first peptide, pref. LFA-1 and
 PT ICAM-1 functional domain derived peptide(s)
 XX
 PS Claim 30; Page 41; 64pp; English.
 XX
 CC Synthetic sub-sequences of ICAM-1 CD54 (AAR80113-24), LFA-1 beta CD18
 CC (AAR80109) or LFA-1 alpha CD18 (AAR80111-12) are used to block
 CC ICAM/LFA binding interaction by binding to a target protein in a
 CC manner that precludes the normal binding reaction between ICAM-1 and
 CC LFA-1. Alternatively, the peptide induces a conformational change
 CC in the target protein, enhancing the reactivity of a second
 CC peptide. The peptides have immunosuppressive appln.
 XX
 SQ Sequence 12 AA;
 Query Match 73.8%; Score 45; DB 16; Length 12;
 St Local Similarity 100.0%; Pred. No. 0.54; Mismatches 0; Indels 0; Gaps 0;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 PRGGSVLVT 10
 |||||||
 Db 3 prggsvlvt 11.
 RESULT 3
 AAR80116
 ID AAR80115 standard; Peptide: 12 AA.
 XX
 AC AAR80116;
 XX
 DT 05-MAR-1996 (first entry)
 DE ICAM CD54 (37-48) peptide SC-3-150.
 DE ICAM-1; CD54; intercellular adhesion molecule-1; integrin; LFA-1;
 KW leucocyte function-associated antigen; immunosuppressive;
 KW SC-3-150.
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 1
 /note= "Ile at position 37 of SC-3-150 is Cys
 at position 1 of SC-3-150"
 PN WO9528170-A1.
 PD 26-OCT-1995.
 PR 19-APR-1994; 94US-0229513.
 PA (UNIV) UNIV KANSAS.
 PI Benedict S, Chan MA, Slahaan TJ, Tibbets SA,
 XX DR WPI; 1995-373631/48.
 XX
 PT Changing peptide reactivity via conjugation with a second peptide -
 PT causes change in conformation of first peptide, pref. LFA-1 and
 PT ICAM-1 functional domain derived peptide(s)
 XX
 PS Claim 30; Page 41; 64pp; English.
 XX
 CC Synthetic sub-sequences of ICAM-1 CD54 (AAR80113-24), LFA-1 beta CD18
 CC (AAR80109) or LFA-1 alpha CD18 (AAR80111-12) are used to block
 CC ICAM/LFA binding interaction by binding to a target protein in a
 CC manner that precludes the normal binding reaction between ICAM-1 and
 CC LFA-1. Alternatively, the peptide induces a conformational change
 CC in the target protein, enhancing the reactivity of a second
 CC peptide. The peptides have immunosuppressive appln.
 XX
 SQ Sequence 12 AA;
 Query Match 73.8%; Score 45; DB 16; Length 12;
 St Local Similarity 100.0%; Pred. No. 0.54; Mismatches 0; Indels 0; Gaps 0;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	2	PRGGSVLVT	10
Db	3	prggsvlvt	11
RESULT	4		
ID	AAW34098	ICAM-1 beta subunit based peptide cIB-C.	
ID	AAW34098 standard; peptide: 12 AA.		
XX			
AC	AAW34098;		
XX			
DT	14-MAY-1998	(first entry)	
XX			
DE	ICAM-1 beta subunit based peptide IB-R.		
XX			
ICAM-1; intracellular adhesion molecule-1; inhibitor; integrin binding;			
KW	lymphocyte fusion associated antigen-1; LFA-1; transplant rejection;		
KW	allergy; autoimmune disease; rheumatoid arthritis; multiple sclerosis;		
KW	insulin-dependent diabetes mellitus; therapy; beta subunit; cyclic;		
XX			
OS	Synthetic.		
OS	Homo sapiens.		
W09741149-A1.			
XX			
PD	06-NOV-1997.		
XX			
FT	Key	Location/Qualifiers	
FT	Disulfide-bond	1:12	
FT	/note-	"form disulphide bond to create cyclic peptide"	
XX			
PN	W09741149-A1.		
XX			
PD	06-NOV-1997.		
XX			
PF	24-APR-1997;	97WO-US06799.	
XX			
PR	23-APR-1997;	97US-0844978.	
PR	26-APR-1996;	96US-0638437.	
PR	26-APR-1996;	96US-0844978.	
XX			
PA	(UNIV) UNIV KANSAS.		
XX			
PI	Benedict S, Chan MA, Siahaan TJ, Tibbatts SA;		
XX			
DR	WPI; 1997-549680/50.		
XX			
PT	Composition of peptide(s) that inhibit binding between proteins -		
PT	used for treatment of transplant rejection, auto:immune disease and		
PT	allergy		
XX			
PS	Claim 5; Page 19; 50pp; English.		
XX			
CC	This sequence represents a cyclic peptide fragment of the beta subunit of		
CC	intracellular adhesion molecule-1 (ICAM-1). This sequence, or a fragment		
CC	of lymphocyte fusion associated antigen-1 (LFA-1), can be used in		
CC	the peptide composition (A) of the invention, which inhibits the binding		
CC	of first and second proteins (P1, P2) and comprises at least one peptide		
CC	that binds to P1 and at least one peptide that binds to P2. (A) is used,		
CC	in vivo or in vitro, to inhibit binding of integrins to their specific		
CC	binding proteins, particularly for treating transplant rejection, allergy		
CC	and autoimmune disease, specifically rheumatoid arthritis,		
CC	insulin-dependent diabetes mellitus and multiple sclerosis.		
XX			
SQ	Sequence 12 AA:		
Query Match	73.8%	Score 45;	DB 18;
Best Local Similarity	100.0%	Pred. No. 0.54;	Length 12;
Matches	9;	Conservative 0;	Mismatches 0;
		Indels 0;	Gaps 0;
RESULT	5		
QY	2	PRGGSVLVT	10
Db	3	prggsvlvt	11
RESULT	6		
QY	2	PRGGSVLVT	10
Db	3	prggsvlvt	11
RESULT	5		
ID	AAW34101	AAW34101 standard; peptide: 11 AA.	
ID	AAW34101	AAW34101 standard; peptide: 12 AA.	
XX			
AC	AAW34101;		

KW TR; KDRE; selenocysteine; arteriosclerosis; diabetes; oedema;
 XX ischaemic lesion.
 OS Homo sapiens.
 XX JPI0309193-A.
 PN
 XX PD 24-NOV-1998.
 XX PF 12-MAY-1997; 97JP-0120443.
 PR 12-MAY-1997; 97JP-0120443.
 XX PA (SANY) SANKYO CO LTD.
 XX DR WPI; 1999-063678/06.
 PT Preparation of a mammalian seleno-cysteine-containing protein in E. coli - useful in the treatment of arteriosclerosis, diabetes, ischaemic lesions and oedema.

PS Example; Page 12; 40pp; Japanese.

XX CC The present sequence represents the C-terminal peptide from human thioredoxin reductase (TR). The TR protein is prepared by gene manipulation and has selenocysteine at position 53 of the mature amino acid sequence. The protein has thioredoxin reducing activity. CC The protein is useful as a preventive and treating agent for CC arteriosclerosis, diabetes, ischaemic lesions, oedema and many other diseases.
 XX SQ Sequence 11 AA;

Query Match	Best Local Similarity	Score	DB	Length
Matches	5; Conservative	30;	20;	11;
	5; Mismatches	1;		
	Indels	3;		
	0;			
	Gaps	0;		

QY 4 GGSVLLVTGC 12
 | | : |
 Db 3 gasilgagc 11

RESULT 7

AAP80452 AAP80452 standard; protein; 5 AA.

ID XX AAC AAW70875;
 ID XX AAW70875 standard; Peptide; 5 AA.
 AC XX AAW70875;
 DT 02-MAR-1999 (first entry)
 DE ICAM-1 peptide fragment possibly recognised by LFA-1.
 KW Intracellular adhesion molecule; ICAM-1; LFA-1; immune response;
 KW inflammation; lymphocyte function-associated antigen; tumour cell;
 KW metastasis; binding ligand; detection; assay; peptide; polypeptide;
 KW immune response; inflammation; immunosuppression.
 XX OS MUS musculus.
 XX US5831036-A.
 XX PD 03-NOV-1998.
 XX PF 25-OCT-1993; 93US-0140554.
 PR 27-APR-1990; 90US-0515478.
 PR 04-MAY-1987; 87US-0045963.
 PR 02-NOV-1987; 87US-0115798.
 PR 16-FEB-1988; 88US-0155943.
 PR 03-MAY-1988; 88US-0189815.
 PR 28-SEP-1988; 88US-0250445.
 PR 16-MAR-1989; 88US-0324481.
 PR 30-JUN-1989; 88US-0373882.
 PR 21-DEC-1989; 88US-0456647.
 PR 25-OCT-1993; 93US-0140554.
 XX (DAND) DANA FARBER CANCER INST INC.
 XX PT Dustin ML, Marlin SD, Rothlein R, Springer TA;
 XX DR WPI; 1998-609323/51.
 PT Soluble fragments of human inter:cellular adhesion molecule 1 -
 PT useful for inhibition of binding of leukocytes in immune responses
 XX e.g. organ transplantation
 PS Example 18; Column 47; 70pp; English.

XX DR WPI; 1989-033081/05.

ICAM-1 fragments obtained from recombinant expression of truncated ICAM-1 coding sequences can be used in the control of adhesion events in inflammatory conditions and immune responses. This is achieved by the ICAM-1 fragments binding to and inhibiting the action of leukocyte surface molecules e.g. LFA-1 which mediate cell-cell adhesion events during immune responses. This inhibition is useful for suppressing immune responses after organ transplantation or skin grafting. Ligands derived from ICAM-1 which are possibly recognised by LFA-1 are described in GENSEQ records AAW0872-W70880.

SQ Sequence 5 AA;

Query Match 45.9%; Score 28; DB 19; Length 5;

Best Local Similarity 100.0%; Pred. No. 6.4e+05; Mismatches 0; Indels 0; Gaps 0; Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PRGG 6

Db 1 prggs 5

RESUL 9

AAR34037

ID AAR34037 standard; peptide; 6 AA.

XX

AC AAR34089;

XX

DT 06 AUG 1993 (first entry)

XX

DE Peptide which binds the ICAM-1 binding site on IRBC.

XX

KW Immunoadhesin; Plasmodium falciparum infected erythrocyte; IRBC;

KW malaria; intercellular adhesion molecule; ICAM-1; CD54;

KW endothelial receptor; antibody.

XX

OS Homo sapiens.

XX

PN W09306850-A.

XX

PD 15-APR-1993.

XX

PF 05-OCT-1992; 92WO-US08484.

XX

PR 03-OCT-1991; 91US-0769625.

PR 03-APR-1992; 92US-0862708.

PR 12-JUN-1992; 92US-0899063.

XX

PA (BLOO-) CENT BLOOD RES.

PA (USSA) US SEC OF ARMY.

XX

PI Ockenhouse CF, Springer TA, Staunton DE;

XX

DR WPI; 1993-134132/716.

XX

PT Inhibition of ICAM-1 binding to malaria-infected erythrocytes -

PT by admin. of ICAM-1 or fragment, antibody etc.; useful in

PT diagnosis or treatment of Plasmodium falciparum malaria

XX

PS Claim 9; Page 49; 67pp; English.

XX

CC The peptide AAR34089 is capable of binding the ICAM-1 binding site on

CC an IRBC. The sequence is shown as a pentapeptide GGSVL in the

CC claims but as the hexapeptide GGSVLV in the sequence listing.

CC See related patents W09306848 and W09306849.

XX

SQ Sequence 6 AA;

RESUL 11

AAR34379

ID AAW34379 standard; peptide; 7 AA.

XX

AC AAW34379;

XX

DT 04-MAR-1998 (first entry)

XX

DE PKB substrate #26.

XX

KW Protein kinase B; PKB; substrate; glycogen metabolism; pancreatic cancer;

KW regulator; protein synthesis; enzyme modulator; type II diabetes;

KW insulin-stimulated crosstide kinase; breast cancer; ovarian cancer;

XX

Query Match 45.9%; Score 28; DB 14; Length 6;

Best Local Similarity 100.0%; Pred. No. 6.4e+05; Mismatches 0; Indels 0; Gaps 0; Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Sequence 6 AA;

The peptide AAR34037 is capable of binding the ICAM-1 binding site on an IRBC. See related patents W09306848 and W09306850.

QY 4 GGSQLV 9

Db 1 ggsvlv 6

OS	Synthetic.	FT	Disulfide-bond	1..?
XX		XX		
XX	WO9722360-A2.	PN	W09557149-A2.	
XX		XX		
PD	26-JUN-1997.	PD	11-NOV-1999.	
XX		XX		
PF	20-DEC-1996;	PR	05-MAY-1999;	99WO-CA00363.
XX	96WO-GB03186.	PR	05-MAY-1998;	98US-0073040.
KW	18-JUL-1996;	PR	06-NOV-1998;	98US-018759.
KW	96GB-0015066.	PR	20-JAN-1999;	99US-024395.
KW	20-DEC-1995;	PR	08-MAR-1999;	99US-0264516.
KW	95GB-0026083.	PA	(ADHE-) ADHEREX TECHNOLOGIES INC.	
KW	16-MAY-1996;	PI	Blaschuk OW, Gour BJ, Byers S;	
KW	96GB-0010272.	DR	WPI; 2000-038791/03.	
PA	(MEDI-) MEDICAL RES COUNCIL.	XX		
PA	(UUDU-) UNIV DUNDEE.	XX		
XX		PS		
PI	Alessi D, Cohen P, Cross D;	PT		
XX		PT		
PS	WPI; 1997-341435/31.	PT		
XX		PT		
CC	Use of protein kinase B for regulation of glycogen metabolism and protein synthesis - also peptide substrates for PKB and methods for screening for modulators	PT		
PT		PT		
XX		PT		
XX		PT		
CC	Example 8: Page 58; 98pp; English.	PT		
CC	This sequence represents a substrate for protein kinase B (PKB). The use of PKB, its analogues, isoforms, inhibitors, activators and/or functional equivalents for regulating glycogen metabolism and/or protein synthesis is the subject of the invention. This sequence can also be used in a method of the invention for identifying agents that modulate the activity of PKB. It can also be used to screen for modulators of enzymes that catalyse PKB phosphorylation. PKB (an insulin-stimulated crosstide kinase) and its analogues etc. are used to treat disease characterised by abnormal glycoxygen metabolism and/or protein synthesis, especially type II diabetes and cancer (specifically of breast, pancreas and ovary). The various screening methods are used to identify agents potentially useful for treating these diseases.	PT		
CC	SQ Sequence 7 AA;	PT		
CC	Query Match 45.9%; Score 28; DB 18; Length 7;	PS	Claim 84; Page 201; 252pp; English.	
CC	Best Local Similarity 100.0%; Pred. No. 6.4e+05;	XX		
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		CC	The present invention describes cadherin modulating agents (MA) comprising peptides which comprise a nonclassical cadherin cell adhesion recognition (CAR) sequence. The MAs can be used for modulating nonclassical cadherin-mediated functions. They can be used for e.g. inhibiting adhesion of nonclassical-cadherin expressing cells in a mammal, enhancing delivery of a drug through the skin of a mammal, enhancing delivery of a drug to a tumour in a mammal, treating cancer in a mammal, inhibiting metastasis of a cancer in a mammal, inhibiting angiogenesis in a mammal, inducing apoptosis in a nonclassical cadherin-expressing cell, preventing or treating obesity in a mammal, stimulating blood vessel reversion in a mammal, enhancing drug delivery to the central nervous system, treating a demyelinating neurological disease, increasing vaso permeability in a mammal, enhancing adhesion of nonclassical-cadherin-expressing cells, inhibiting synaptic stability in a mammal, or preventing pregnancy in a mammal. They can also be used for e.g. enhancing or directing neurite outgrowth, facilitating wound healing or reducing scar tissue, or enhancing adhesion of foreign tissue in a mammal. They can also be used for treating e.g. psoriasis, arthritis, age-related macular degeneration, multiple sclerosis and diabetes. The products can also be used for detection and diagnosis and in bioreactors. AAY64592 to AAY64572 represent specifically claimed peptides, and AAY64573 to AAY4643 and AA233183 to AA233186 represent sequences used in the exemplification of the present invention.	
CC	SQ Sequence 7 AA;	XX		
CC	Query Match 45.9%; Score 28; DB 21; Length 7;	PS		
CC	Best Local Similarity 100.0%; Pred. No. 6.4e+05;	XX		
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		CC		
CC	DT 02-MAR-2000 (first entry)	Db	RESULT 13	
DE	Protocadherin cell adhesion recognition cyclic peptide SEQ ID NO:2718.	Db	8 LVTGC 12	
XX		Db	3 lvtgc 7	
XX		XX		
KW	Modulation; nonclassical cadherin mediated cell adhesion; CAR;	XX		
KW	inhibition; cadherin extracellular domain; cell adhesion recognition;	XX		
KW	OB-cadherin; cadherin-5; cadherin-6; cadherin-7; cadherin-8;	XX		
KW	cadherin-12; cadherin-14; cadherin-15; T-cadherin; P-cadherin;	XX		
KW	desmoglein; desmocollin; calcium binding; cancer; tumour; obesity;	XX		
KW	rheumatoid arthritis; multiple sclerosis; diabetes; metastasis;	XX		
XX	neurological disease; cyclic.	XX		
OS	Synthetic.	XX		
OS	Homo sapiens.	XX		
XX		XX		
FH	Key Location/Qualifiers	XX		
KW	Modulation; nonclassical cadherin mediated cell adhesion; CAR;	XX		

KW inhibition; cadherin extracellular domain; cell adhesion recognition;
KW OB-cadherin; cadherin-5; cadherin-6; cadherin-7; cadherin-8;
KW cadherin-12; cadherin-14; cadherin-15; T-cadherin; PB-cadherin;
KW cadherin related neuronal receptor; li-cadherin; protocadherin;
KW desmoglein; desmocollin; calcium binding; cancer; tumour; obesity;
KW rheumatoid arthritis; multiple sclerosis; diabetes; metastasis;
KW neurological disease; cyclic.
OS Synthetic.
OS Homo sapiens.
FH Key Location/Qualifiers
FT disulfide-bond 1..8
XX
PA (ADHE-) ADHEREX TECHNOLOGIES INC.
XX
PT Blaschuk OW, Gour BJ, Byers S;
DR WPI; 2000-038791/03.
XX
PS Claim 84; Page 201; 252pp; English.
CC The present invention describes cadherin modulating agents (MA) comprising peptides which comprise a nonclassical cadherin cell adhesion recognition (CAR) sequence. The MAs can be used for modulating nonclassical cadherin-mediated functions. They can be used for e.g. inhibiting adhesion of nonclassical-cadherin expressing cells in a mammal, enhancing delivery of a drug through the skin of a mammal, enhancing delivery of a drug to a tumour in a mammal, treating cancer in a mammal, inhibiting metastasis of a cancer in a mammal, inhibiting angiogenesis in a mammal, inducing apoptosis in a nonclassical cadherin-expressing cell, preventing or treating obesity in a mammal, stimulating blood vessel regression in a mammal, enhancing drug delivery to the central nervous system, treating a demyelinating neurological disease, increasing vaso permeability in a mammal, enhancing adhesion of nonclassical cadherin-expressing cells, inhibiting synaptic stability in a mammal, or preventing pregnancy in a mammal. They can also be used for e.g. enhancing or directing neurite outgrowth, facilitating wound healing or reducing scar tissue, or enhancing adhesion of foreign tissue in a mammal. They can also be used for treating e.g. psoriasis, arthritis, age-related macular degeneration, multiple sclerosis and diabetes. The products can also be used for detection and diagnosis and in bioreactors. AAY60592 to AAY64572 represent specifically claimed peptides, and AAY64573 to AAY6643 and AAY233183 represent sequences used in the exemplification of the present invention.
CC Sequence 8 AA;
CC Query Match 45.9%; Score 28; DB 21; Length 8;
CC Best Local Similarity 100.0%; Pred. No. 6.4e+05; Matches 5; Conservative 0; Mismatches 0; Indels 0; Caps 0;
Qy 8 LYTGIC 12
Db 4 lvtgc 8

RESULT 14
ID AAY63240 standard; Peptide; 9 AA.
AC AAY63240;
XX
DT 02-MAR-2000 (first entry)
XX
DE Protocadherin cell adhesion recognition cyclic peptide SEQ ID NO:2724.
XX
Modulation: nonclassical cadherin mediated cell adhesion; CAR:
KW inhibition; cadherin extracellular domain; cell adhesion recognition;
KW OB-cadherin; cadherin-5; cadherin-6; cadherin-7; cadherin-8;
KW cadherin-12; cadherin-14; cadherin-15; T-cadherin; PB-cadherin;
KW cadherin related neuronal receptor; li-cadherin; protocadherin;
KW desmoglein; desmocollin; calcium binding; cancer; tumour; obesity;
KW rheumatoid arthritis; multiple sclerosis; diabetes; metastasis;
KW neurological disease; cyclic.
OS Synthetic.
OS Homo sapiens.
FH Key Location/Qualifiers
FT disulfide-bond 1..9
XX
PA (ADHE-) ADHEREX TECHNOLOGIES INC.
XX
PT Blaschuk OW, Gour BJ, Byers S;
DR WPI; 2000-038791/03.
XX
PS Claim 84; Page 201; 252pp; English.
CC The present invention describes cadherin modulating agents (MA) comprising peptides which comprise a nonclassical cadherin cell adhesion recognition (CAR) sequence. The MAs can be used for modulating nonclassical cadherin-mediated functions. They can be used for e.g. inhibiting adhesion of nonclassical-cadherin expressing cells in a mammal, enhancing delivery of a drug through the skin of a mammal, enhancing delivery of a drug to a tumour in a mammal, treating cancer in a mammal, inhibiting metastasis of a cancer in a mammal, inhibiting angiogenesis in a mammal, inducing apoptosis in a nonclassical cadherin-expressing cell, preventing or treating obesity in a mammal, stimulating blood vessel regression in a mammal, enhancing drug delivery to the central nervous system, treating a demyelinating neurological disease, increasing vaso permeability in a mammal, enhancing adhesion of nonclassical cadherin-expressing cells, inhibiting synaptic stability in a mammal, or preventing pregnancy in a mammal. They can also be used for e.g. enhancing or directing neurite outgrowth, facilitating wound healing or reducing scar tissue, or enhancing adhesion of foreign tissue in a mammal. They can also be used for treating e.g. psoriasis, arthritis, age-related macular degeneration, multiple sclerosis and diabetes. The products can also be used for detection and diagnosis and in bioreactors. AAY60592 to AAY64572 represent specifically claimed peptides, and AAY64573 to AAY6643 and AAY233183 to AAY233186 represent sequences used in the exemplification of the present invention.

XX SQ Sequence 9 AA;

CC central nervous system, treating a demyelinating neurological disease,

CC increasing vaso permeability in a mammal, enhancing adhesion of

CC nonclassical cadherin-expressing cells, inhibiting synaptic stability in

CC a mammal, or preventing pregnancy in a mammal. They can also be used for

CC e.g. enhancing or directing neurite outgrowth, facilitating wound

CC healing or reducing scar tissue, or enhancing adhesion of foreign tissue

CC in a mammal. They can also be used for treating e.g. psoriasis,

CC arthritis, age-related macular degeneration, multiple sclerosis and

CC diabetes. The products can also be used for detection and diagnosis and

CC in bioreactors. AAY60502 to AAY64572 represent specifically claimed

CC peptides, and AAY4573 to AAY64613 and AAZ33183 to AAZ33186 represent

CC sequences used in the exemplification of the present invention.

RESULT 15

AN163243 SQ

ID AAV63243 standard; Peptide: 10 AA.

XX AC AAY63243;

XX DE 02-MAR-2000 (first entry)

DE Protocadherin cell adhesion recognition cyclic peptide SEQ ID NO:2727.

XX KW Modulation; nonclassical cadherin mediated cell adhesion; CAR;

KW inhibition; cadherin extracellular domain; cell adhesion recognition;

KW OB-cadherin; cadherin-5; cadherin-6; cadherin-7; cadherin-8;

KW cadherin-12; cadherin-14; cadherin-15; T-cadherin; PB-cadherin;

KW cadherin related neuronal receptor; LI-cadherin; protocadherin;

KW desmoglein; desmocollin; calcium binding; cancer; tumour; obesity;

KW rheumatoid arthritis; multiple sclerosis; diabetes; metastasis;

KW neurological disease; cyclic.

XX OS Synthetic.

XX OS Homo sapiens.

XX Key Location/Qualifiers

FH Disulfide-bond 1..10

XX FT WO957149-A2.

XX PD 11-NOV-1999.

XX PR 05-MAY-1999; 99WO-CA00363.

PR 05-MAY-1998; 98US-0073040.

PR 06-NOV-1998; 98US-0187859.

PR 20-JAN-1999; 99US-0234395.

PR 08-MAR-1999; 99US-0264516.

PA (ADHE-) ADHEREX TECHNOLOGIES INC.

XX PI Blaschuk OW, Gour BJ, Byers S;

XX DR WPI; 2000-038791/03.

XX PT New cadherin modulating agents, used for modulating nonclassical

PT cadherin-mediated functions for treating e.g. cancers, obesity,

PT rheumatoid arthritis, multiple sclerosis, diabetes or a neurological

PT disease -

XX PS Claim 84; Page 201; 252pp; English.

XX CC The present invention describes cadherin modulating agents (MA)

CC comprising peptides which comprise a nonclassical cadherin cell adhesion

CC recognition (CAR) sequence. The MAs can be used for modulating

CC nonclassical cadherin-mediated functions. They can be used for e.g.

CC inhibiting adhesion of nonclassical-cadherin expressing cells in a

CC mammal, enhancing delivery of a drug through the skin of a mammal,

CC a mammal, inhibiting metastasis of a cancer in a mammal, inhibiting

CC angiogenesis in a mammal, inducing apoptosis in a nonclassical cadherin-

CC expressing cell, preventing or treating obesity in a mammal, stimulating

CC blood vessel regression in a mammal, enhancing drug delivery to the

GenCore version 4.5
 Copyright (c) 1993 - 2000 compugen Ltd.
OM protein - protein search, using sw model
Run on: October 10, 2002, 06:20:47 ; **Search time** 23.52 Seconds
(without alignments) **Number of cell updates/sec** 12.462

Title: US-09-629-719D-8
Perfect score: 61
Sequence: 1 XPRGGSVLVTGC 12
Scoring table: BLOSUM62
Gapop 10.0 , **Gapext** 0.5

Searched: 231628 seqs, 2425594 residues

Total number of hits satisfying chosen parameters: 83765

Minimum DB seq length: 0

Maximum DB seq length: 12

Post-processing: Maximum Match 0%
 Listing first 45 summaries

Database :

Issued_Patents_AA: *

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 2: /cgn2_6/podata/2/1aa/5B_COMB.pep: *
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 4: /cgn2_6/podata/2/1aa/6B_COMB.pep: *
 5: /cgn2_6/podata/2/1aa/PCBTS_COMB.pep: *
 6: /cgn2_6/podata/2/1aa/backfiles1.pep: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

ALIGNMENTS

RESULT 1

US-08-789-078-9

Sequence 9, Application US/08789078
 Patent No. 5843885

GENERAL INFORMATION:

APPLICANT: Benedict, Stephen H.

APPLICANT: Siahraen, Teruna

APPLICANT: Chan, Marcia

APPLICANT: Tibbetts, Scott

TITLE OF INVENTION: ICAM-1/LFA-1 PEPTIDES FOR INDUCING IMMUNE TOLERANCE

NUMBER OF SEQUENCES: 19

CORRESPONDENCE ADDRESS:

ADDRESSEE: HOVEL, WILLIAMS, TIMMONS & COLLINS

STREET: 1101 Walnut St.

CITY: Kansas City

STATE: MO

COUNTRY: USA

ZIP: 64105

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/789,078

FILING DATE: 03-FEB-1997

CLASSIFICATION: 514

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/229,513

FILING DATE: 19-APR-1994

ATTORNEY/AGENT INFORMATION:

NAME: Collins, John M.

REGISTRATION NUMBER: 26262

REFERENCE/DOCKET NUMBER: 22833

TELECOMMUNICATION INFORMATION:

TELEPHONE: (816)474-9050

TELEX: 431-363

INFORMATION FOR SEQ ID NO: 9:

SEQUENCE CHARACTERISTICS:

LENGTH: 11 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: peptide

HYPOTHETICAL: NO

FRAGMENT TYPE: Internal

ORIGINAL SOURCE:

ORGANISM: Homo sapiens

CELL TYPE: T-cell

; US-08-789-078-9
CELL LINE: HL-60

RESULT 3

PCT-US95-04886-9

; Sequence 9, Application PC/TU9504886

; GENERAL INFORMATION:

; APPLICANT: Benedict, Stephen H.

; APPLICANT: Siahaan, Teruna

; APPLICANT: Chan, Marcia

; APPLICANT: Tibbetts, Scott

; TITLE OF INVENTION: ICAM-1/LFA-1 PEPTIDES FOR INDUCING

; NUMBER OF SEQUENCES: 19

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: HOVEY, WILLIAMS, TIMMONS & COLLINS

; STREET: 1101 Walnut St.

; CITY: Kansas City

; STATE: MO

; COUNTRY: USA

; ZIP: 64106

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent In Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/752,633

; FILING DATE:

; CLASSIFICATION: 514

; ATTORNEY/AGENT INFORMATION:

; NAME: Collins, John M.

; REFERENCE/DOCKET NUMBER: 26262

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (816)474-9050

; TELEFAX: 816)474-9057

; TELEX: 434-363

; INFORMATION FOR SEQ ID NO: 9:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 11 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

; HYPOTHETICAL: NO

; FRAGMENT TYPE: Internal

; ORIGINAL SOURCE:

; ORGANISM: Homo sapiens

; CELL TYPE: T-cell

; CELL LINE: HL-60

; PCT-US95-04886-9

; Query Match

; Best Local Similarity 83.6%; Score 51; DB 2; Length 11;

; Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

; Sequence 7, Application US/08752,633

; Patent No. 5843885

; GENERAL INFORMATION:

; APPLICANT: Benedict, Stephen H.

; APPLICANT: Siahaan, Teruna

; APPLICANT: Chan, Marcia

; APPLICANT: Tibbetts, Scott

; TITLE OF INVENTION: ICAM-1/LFA-1 PEPTIDES FOR INDUCING

; NUMBER OF SEQUENCES: 19

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: HOVEY, WILLIAMS, TIMMONS & COLLINS

; STREET: 1101 Walnut St.

; CITY: Kansas City

; STATE: MO

; COUNTRY: USA

; ZIP: 64106

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent In Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: PCT/US95/04886

; FILING DATE:

; CLASSIFICATION:

; ATTORNEY/AGENT INFORMATION:

; NAME: Collins, John M.

; REFERENCE/DOCKET NUMBER: 26262

; TELECOMMUNICATION INFORMATION:

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; TELEFAX: 816)474-9057

; TELEX: 434-363

; INFORMATION FOR SEQ ID NO: 9:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 11 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

; HYPOTHETICAL: NO

; FRAGMENT TYPE: Internal

; ORIGINAL SOURCE:

; ORGANISM: Homo sapiens

; CELL TYPE: T-cell

; CELL LINE: HL-60

; PCT-US95-04886-9

; Query Match

; Best Local Similarity 83.6%; Score 51; DB 2; Length 11;

; Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

; Sequence 7, Application US/08752,633

; Patent No. 5843885

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; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent In Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: PCT/US95/04886

; FILING DATE:

; CLASSIFICATION:

; ATTORNEY/AGENT INFORMATION:

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; TELEPHONE: (816)474-9050

; TELEFAX: 816)474-9057

; TELEX: 434-363

; INFORMATION FOR SEQ ID NO: 9:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 11 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

; HYPOTHETICAL: NO

; FRAGMENT TYPE: Internal

; ORIGINAL SOURCE:

; ORGANISM: Homo sapiens

; CELL TYPE: T-cell

; CELL LINE: HL-60

; PCT-US95-04886-9

; Query Match

; Best Local Similarity 83.6%; Score 51; DB 2; Length 11;

; Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

; Sequence 7, Application US/08752,633

; Patent No. 5843885

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; STATE: MO

; COUNTRY: USA

; ZIP: 64106

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent In Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: PCT/US95/04886

; FILING DATE:

; CLASSIFICATION:

; ATTORNEY/AGENT INFORMATION:

; NAME: Collins, John M.

; REFERENCE/DOCKET NUMBER: 26262

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (816)474-9050

; TELEFAX: 816)474-9057

; TELEX: 434-363

; INFORMATION FOR SEQ ID NO: 9:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 11 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

; HYPOTHETICAL: NO

; FRAGMENT TYPE: Internal

; ORIGINAL SOURCE:

; ORGANISM: Homo sapiens

; CELL TYPE: T-cell

; CELL LINE: HL-60

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; Query Match

; Best Local Similarity 83.6%; Score 51; DB 2; Length 11;

; Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

; Sequence 7, Application US/08752,633

; Patent No. 5843885

; GENERAL INFORMATION:

; APPLICANT: Benedict, Stephen H.

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; APPLICANT: Chan, Marcia

; APPLICANT: Tibbetts, Scott

; TITLE OF INVENTION: ICAM-1/LFA-1 PEPTIDES FOR INDUCING

; NUMBER OF SEQUENCES: 19

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: HOVEY, WILLIAMS, TIMMONS & COLLINS

; STREET: 1101 Walnut St.

; CITY: Kansas City

; STATE: MO

; COUNTRY: USA

; ZIP: 64106

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent In Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: PCT/US95/04886

; FILING DATE:

; CLASSIFICATION:

; ATTORNEY/AGENT INFORMATION:

; NAME: Collins, John M.

; REFERENCE/DOCKET NUMBER: 26262

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (816)474-9050

; TELEFAX: 816)474-9057

; TELEX: 434-363

; INFORMATION FOR SEQ ID NO: 9:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 11 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

; HYPOTHETICAL: NO

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; ORIGINAL SOURCE:

; ORGANISM: Homo sapiens

; CELL TYPE: T-cell

; CELL LINE: HL-60

; PCT-US95-04886-9

; Query Match

; Best Local Similarity 83.6%; Score 51; DB 2; Length 11;

; Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

; Sequence 7, Application US/08752,633

; Patent No. 5843885

; GENERAL INFORMATION:

; APPLICANT: Benedict, Stephen H.

; APPLICANT: Siahaan, Teruna

; APPLICANT: Chan, Marcia

; APPLICANT: Tibbetts, Scott

; TITLE OF INVENTION: ICAM-1/LFA-1 PEPTIDES FOR INDUCING

; NUMBER OF SEQUENCES: 19

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: HOVEY, WILLIAMS, TIMMONS & COLLINS

; STREET: 1101 Walnut St.

; CITY: Kansas City

; STATE: MO

; COUNTRY: USA

; ZIP: 64106

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent In Release #1.0, Version #1.25

STREET: 1101 Walnut St.
 CITY: Kansas City
 STATE: MO
 COUNTRY: USA
 ZIP: 64106
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/789,078
 FILING DATE: 03-FEB-1997
 CLASSIFICATION: 514
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: 08/229,513
 FILING DATE: 19-APR-1994
 ATTORNEY/AGENT INFORMATION:
 NAME: Collins, John M.
 REGISTRATION NUMBER: 26262
 REFERENCE/DOCKET NUMBER: 22833
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (816)474-9050
 TELEX: 434 363
 INFORMATION FOR SEQ ID NO: 7:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 12 amino acids
 TYPE: amino acid
 MOLECULE TYPE: peptide
 HYPOTHETICAL: NO
 FRAGMENT TYPE: internal
 ORIGINAL SOURCE:
 ORGANISM: Homo sapiens
 CELL TYPE: T-cell
 LENGTH: 12 amino acids
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 HYPOTHETICAL: NO
 FRAGMENT TYPE: internal
 ORIGINAL SOURCE:
 ORGANISM: Homo sapiens
 CELL TYPE: T-cell
 CELL LINE: HL-60
 US-08-789-078-7

Query Match 73.8%; Score 45; DB 2; Length 12;
 Best Local Similarity 100.0%; Pred. No. 0.13; Mismatches 0;
 Matches 9; Conservative 0; MisMatches 0; Indels 0; Gaps 0;

Qy 2 PRGGSVLVT 10
 Db 3 PRGGSVLVT 11

RESULT 5 US-08-789-078-8
 Query Match 73.8%; Score 45; DB 2; Length 12;
 Best Local Similarity 100.0%; Pred. No. 0.13; Mismatches 0;
 Matches 9; Conservative 0; MisMatches 0; Indels 0; Gaps 0;
 Qy 2 PRGGSVLVT 10
 Db 3 PRGGSVLVT 11

RESULT 6 US-08-752-633-7
 Query Match 73.8%; Score 45; DB 2; Length 12;
 Best Local Similarity 100.0%; Pred. No. 0.13; Mismatches 0;
 Matches 9; Conservative 0; MisMatches 0; Indels 0; Gaps 0;
 Patient No. 5863889
 GENERAL INFORMATION:
 APPLICANT: Benedict, Stephen H.
 APPLICANT: Sianian, Teruna
 APPLICANT: Chan, Marcia
 APPLICANT: Tibbets, Scott
 TITLE OF INVENTION: ICAM-1/LFA-1 PEPTIDES FOR INDUCING
 TITLE OF INVENTION: IMMUNE TOLERANCE
 NUMBER OF SEQUENCES: 19
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: HOVEY, WILLIAMS, TIMMONS & COLLINS
 STREET: 1101 Walnut St.
 CITY: Kansas City
 STATE: MO
 COUNTRY: USA
 ZIP: 64106
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/752,633
 FILING DATE:
 CLASSIFICATION: 514
 ATTORNEY/AGENT INFORMATION:
 NAME: Collins, John M.
 REGISTRATION NUMBER: 26262
 REFERENCE/DOCKET NUMBER: 22833
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (816)474-9050

Query Match 73.8%; Score 45; DB 2; Length 12;
 Best Local Similarity 100.0%; Pred. No. 0.13; Mismatches 0;
 Matches 9; Conservative 0; MisMatches 0; Indels 0; Gaps 0;
 Patient No. 5863885
 GENERAL INFORMATION:
 APPLICANT: Benedict, Stephen H.
 APPLICANT: Sianian, Teruna
 APPLICANT: Chan, Marcia
 APPLICANT: Tibbets, Scott
 TITLE OF INVENTION: ICAM-1/LFA-1 PEPTIDES FOR INDUCING
 TITLE OF INVENTION: IMMUNE TOLERANCE
 NUMBER OF SEQUENCES: 19
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: HOVEY, WILLIAMS, TIMMONS & COLLINS
 STREET: 1101 Walnut St.
 CITY: Kansas City
 STATE: MO
 COUNTRY: USA
 ZIP: 64106
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/752,633
 FILING DATE:
 CLASSIFICATION: 514
 ATTORNEY/AGENT INFORMATION:
 NAME: Collins, John M.
 REGISTRATION NUMBER: 26262
 REFERENCE/DOCKET NUMBER: 22833
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (816)474-9050

TELEFAX: 816)474-9057
TELEX: 434-353
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
TOPOLGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
FRAGMENT TYPE: Internal
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
CELL TYPE: T-cell
CELL LINE: HL-60
US-08-752-633-7

RESULT 7
Query Match 73.8%; Score 45; DB 2; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 9; Conservative 0; Mismatches 0;
Indels 0; Gaps 0;
Qy 2 PRGGSVLVT 10
Db 3 PRGGSVLVT 11

RESULT 8
Query Match 73.8%; Score 45; DB 2; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 9; Conservative 0; Mismatches 0;
Indels 0; Gaps 0;
Qy 2 PRGGSVLVT 10
Db 3 PRGGSVLVT 11

RESULT 7
Query Match 73.8%; Score 45; DB 2; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 9; Conservative 0; Mismatches 0;
Indels 0; Gaps 0;
Qy 2 PRGGSVLVT 10
Db 3 PRGGSVLVT 11

RESULT 7
Sequence 8 Application US/08752633
Patent No. 5863889
GENERAL INFORMATION:
APPLICANT: Benedict, Stephen H.
APPLICANT: Sianahan, Teruna
APPLICANT: Chan, Marcia
TITLE OF INVENTION: ICAM-1/LFA-1 PEPTIDES FOR INDUCING
NUMBER OF SEQUENCES: IMMUNE TOLERANCE 19

CORRESPONDENCE ADDRESS:
ADDRESSEE: HOVEY, WILLIAMS, TIMMONS & COLLINS
STREET: 1101 Walnut St.
CITY: Kansas City
STATE: MO
COUNTRY: USA
ZIP: 64106
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patientin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/752,633
FILING DATE: 1998-02-10
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Collins, John M.
REGISTRATION NUMBER: 26262
REFERENCE/DOCKET NUMBER: 24769-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (816)474-9050
TELEFAX: 816)474-9057
TELEX: 434-363
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
TYPE: amino acid
TOPOLGY: linear
MOLECULE TYPE: peptide
US-08-844-978-4

RESULT 7
Sequence 8 Application US/08844978
Patent No. 6075004
GENERAL INFORMATION:
APPLICANT: Benedict, Stephen H.
APPLICANT: Sianahan, Teruna
APPLICANT: Chan, Marcia
TITLE OF INVENTION: Peptide Compositions Which Induce Immune
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: HOVEY, WILLIAMS, TIMMONS & COLLINS
STREET: 2405 Grand Boulevard, Suite 400
CITY: Kansas City
STATE: MO
COUNTRY: USA
ZIP: 64108
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patientin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/844,978
FILING DATE: 1998-02-10
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Collins, John M.
REGISTRATION NUMBER: 26262
REFERENCE/DOCKET NUMBER: 24769-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (816)474-9050
TELEFAX: 816)474-9057
TELEX: 434-363
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
TYPE: amino acid
TOPOLGY: linear
MOLECULE TYPE: peptide
US-08-844-978-4

RESULT 9
Query Match 73.8%; Score 45; DB 3; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 9; Conservative 0; Mismatches 0;
Indels 0; Gaps 0;
Qy 2 PRGGSVLVT 10
Db 3 PRGGSVLVT 11

RESULT 9
Sequence 7 Application US/08844978
Patent No. 6075004
GENERAL INFORMATION:
APPLICANT: Benedict, Stephen H.
APPLICANT: Sianahan, Teruna
APPLICANT: Chan, Marcia
TITLE OF INVENTION: Peptide Compositions Which Induce Immune
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: HOVEY, WILLIAMS, TIMMONS & COLLINS
STREET: 2405 Grand Boulevard, Suite 400
CITY: Kansas City
STATE: MO
COUNTRY: USA
ZIP: 64108
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patientin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/844,978
FILING DATE: 1998-02-10
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Collins, John M.
REGISTRATION NUMBER: 26262
REFERENCE/DOCKET NUMBER: 24769-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (816)474-9050
TELEFAX: 816)474-9057
TELEX: 434-363
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
TYPE: amino acid
TOPOLGY: linear
MOLECULE TYPE: peptide
US-08-844-978-4

APPLICANT: Chan, Marcia
 APPLICANT: Tibbets, Scott
 TITLE OF INVENTION: Peptide Compositions Which Induce Immune
 NUMBER OF SEQUENCES: 36
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: HOVEY, WILLIAMS, TIMMONS & COLLINS
 STREET: 2405 Grand Boulevard, Suite 400
 CITY: Kansas City
 STATE: MO
 COUNTRY: USA
 ZIP: 64108

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/844,978
 FILING DATE: CLASSIFICATION: 514
 ATTORNEY/AGENT INFORMATION:
 NAME: Collins, John M.

REGISTRATION NUMBER: 26262
 REFERENCE/DOCKET NUMBER: 24769-A
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (816)474-9050
 TELEFAX: 816474-9057
 TELEX: 434-363

INFORMATION FOR SEQ ID NO: 7:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 12 amino acids
 TYPE: amino acid
 TOPOLOGY: circular
 LENGTH: 12 amino acids
 MOLECULE TYPE: peptide

US-08-844-978-7

REFERENCE/DOCKET NUMBER: 26262
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (816)474-9050
 TELEFAX: 816474-9057
 TELEX: 434-363

INFORMATION FOR SEQ ID NO: 7:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 12 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 LENGTH: 12 amino acids
 MOLECULE TYPE: peptide
 HYPOTHETICAL: No
 FRAGMENT TYPE: internal
 ORIGINAL SOURCE: Homo sapiens
 ORGANISM: Homo sapiens
 CELL TYPE: T-cell
 CELL LINE: HL-60

PCT-US95-04886-7

Query Match 73.8%; Score 45; DB 3; Length 12;
 Best Local Similarity 100.0%; Pred. No. 0.13; Mismatches 0;
 Matches 9; Conservative 0; Indels 0; Gaps 0;

Qy	2 PRGGSVLVT 10	Db	3 PRGGSVLVT 11

RESULT 11
 PCT-US95-04886-8
 Sequence 8, Application PC/TUS9504886
 GENERAL INFORMATION:

GENERAL INFORMATION:
 APPLICANT: Benedict, Stephen H.

APPLICANT: Siahaan, Teruna

APPLICANT: Chan, Marcia

APPLICANT: Tibbets, Scott

TITLE OF INVENTION: ICAM-1/LFA-1 PEPTIDES FOR INDUCING
 NUMBER OF SEQUENCES: 19

NUMBER OF SEQUENCES: 19
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: HOVEY, WILLIAMS, TIMMONS & COLLINS

STREET: 1101 Walnut St.

CITY: Kansas City

STATE: MO

COUNTRY: USA

ZIP: 64106

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: PCT/US95/04886
 FILING DATE: CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:
 NAME: Collins, John M.

REGISTRATION NUMBER: 26262
 REFERENCE/DOCKET NUMBER: 22833
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (816)474-9050
 TELEFAX: 816474-9057
 TELEX: 434-363

INFORMATION FOR SEQ ID NO: 8:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 12 amino acids
 TYPE: amino acid
 TOPOLOGY: cyclic
 MOLECULE TYPE: peptide

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: PCT/US95/04886
 FILING DATE: CLASSIFICATION:

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; HYPOTHETICAL: NO
; FRAGMENT TYPE: Internal
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; CELL TYPE: T-cell
; CELL LINE: HL-60
; PCP-US95-04886-8

; RESULT 14
; Query Match 73.8%; Score 45; DB 5; Length 12;
; Best Local Similarity 100.0%; Pred. No. 0.13; Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
; Sequence 2721, Application US/09187859A
; Patent No. 6358920
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
; TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS
; FILE REFERENCE: 100086.407CL
; CURRENT APPLICATION NUMBER: US/09/187,859A
; CURRENT FILING DATE: 1998-11-06
; NUMBER OF SEQ ID NOS: 4052
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2721
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Representative cyclic modulating agent based on
; OTHER INFORMATION: Protocadherin cell adhesion recognition sequence
; US-09-187-859-2721

; RESULT 15
; Query Match 45.9%; Score 28; DB 6; Length 5;
; Best Local Similarity 100.0%; Pred. No. 1.7e+05; Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
; Sequence 2724, Application US/09187859A
; Patent No. 6358920
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
; TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS
; FILE REFERENCE: 100086.407CL
; CURRENT APPLICATION NUMBER: US/09/187,859A
; CURRENT FILING DATE: 1998-11-06
; NUMBER OF SEQ ID NOS: 4052
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2724
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Representative cyclic modulating agent based on
; OTHER INFORMATION: Protocadherin cell adhesion recognition sequence
; US-09-187-859-2724

; RESULT 13
; Query Match 45.9%; Score 28; DB 6; Length 5;
; Best Local Similarity 100.0%; Pred. No. 1.7e+05; Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
; Sequence 2718, Application US/09187859A
; Patent No. 6358920
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
; TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS
; FILE REFERENCE: 100086.407CL
; CURRENT APPLICATION NUMBER: US/09/187,859A
; CURRENT FILING DATE: 1998-11-06
; NUMBER OF SEQ ID NOS: 4052
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2718
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Representative cyclic modulating agent based on
; OTHER INFORMATION: Protocadherin cell adhesion recognition sequence
; US-09-187-859-2718

Query Match 45.9%; Score 28; DB 4; Length 7;
; Best Local Similarity 100.0%; Pred. No. 1.7e+05; Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
; OTHER INFORMATION: Representative cyclic modulating agent based on
; OTHER INFORMATION: Protocadherin cell adhesion recognition sequence
; US-09-187-859-2718

Qy 8 LVTGC 12
Db 5 LVTGC 9

; RESULT 14
; Query Match 45.9%; Score 28; DB 4; Length 9;
; Best Local Similarity 100.0%; Pred. No. 1.7e+05; Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
; Sequence 2721, Application US/09187859A
; Patent No. 6358920
; GENERAL INFORMATION:
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
; TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS
; FILE REFERENCE: 100086.407CL
; CURRENT APPLICATION NUMBER: US/09/187,859A
; CURRENT FILING DATE: 1998-11-06
; NUMBER OF SEQ ID NOS: 4052
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2721
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Representative cyclic modulating agent based on
; OTHER INFORMATION: Protocadherin cell adhesion recognition sequence
; US-09-187-859-2721

; Search completed: October 10, 2002, 06:20:47
; Job time: 368 sec

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